

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2006, 12:04:21 ; Search time 301 Seconds  
(without alignments)  
510.141 Million cell updates/sec

Title: US-09-716-395-2

Perfect score: 897  
Sequence: 1 MAHAGRTGYDNRIVMKYIH.....WIQDNGWDFAVELYGPSMR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	769.5	85.8	239	1 BCL2 HUMAN	P10415 homo sapien
2	767.5	85.6	229	1 BCL2 BOVIN	O02718 bos taurus
3	766.5	85.5	235	2 Q81008 FELCA	Q81008 felis silve
4	766	85.4	236	1 BCL2 RAT	P49950 rattus norv
5	765.5	85.3	239	2 Q75SV7 CANPA	Q75SV7 canis faml
6	757	84.4	236	2 Q4VBF6 MOUSE	Q4VBF6 mus musculu
7	757	84.4	236	2 Q7TSN8 RAT	Q7TSN8 rattus norv
8	757	84.4	236	2 Q8BQK4 MOUSE	Q8BQK4 mus musculu
9	752	83.8	236	1 BCL2 CRIGR	Q9JJV8 cricetulus
10	752	83.8	236	1 BCL2 MOUSE	P10417 mus musculu
11	752	83.8	236	2 Q923R6 CRILLO	Q923R6 cricetulus
12	749	83.5	236	2 Q6R755 CANPA	Q6R755 canis faml
13	712.5	79.4	185	2 Q8MJ81 BOVIN	Q8MJ81 bos taurus
14	710.5	79.2	233	1 BCL2 CHICK	Q00709 gallus gall
15	694	77.4	199	2 Q6NTH7 MOUSE	Q6NTH7 mus musculu
16	606	67.6	133	2 Q7YRB6 CANPA	Q7YRB6 canis faml
17	556	62.0	166	2 Q6R7E0 MESAU	Q6R7E0 mesocricetu
18	545	60.8	209	2 Q462R3 BOVIN	Q462R3 bos taurus
19	529	59.0	233	2 Q5C289 HUMAN	Q5C289 homo sapien
20	527	58.8	205	2 Q5T564 HUMAN	Q5T564 homo sapien
21	527	58.8	233	1 BCLX HUMAN	Q07817 homo sapien
22	527	58.8	233	2 Q5T565 HUMAN	Q5T565 homo sapien
23	527	58.8	233	2 Q8SQ42 FELCA	Q8SQ42 felis silve
24	527	58.8	233	2 Q9N1A2 PIG	Q9N1A2 sus scrofa
25	525	58.5	233	2 Q9M2S7 SHEEP	Q9M2S7 ovis aries
26	524	58.4	233	1 BCLX PIG	Q77737 sus scrofa
27	522	58.2	233	1 Q9MYW4 RABIT	Q9MYW4 oryctolagus
28	515	57.4	233	1 BCLX MOUSE	Q64373 mus musculu
29	511	57.0	233	2 Q5H2H3 MOUSE	Q5H2H3 mus musculu
30	511	57.0	233	1 BCLX RAT	P53563 rattus norv
31	509	56.7	233	1 BCLX RAT	P53563 rattus norv

#### RESULT 1

BCL2 HUMAN

ID BCL2 HUMAN STANDARD; PRT; 239 AA.

AC P10415; P10416; Q13842; Q16197;

DT 01-JUL-1989, integrated into UniProtKB/Swiss-Prot.

DT 01-APR-1993, sequence version 85.

DT 07-MAR-2006, entry version 85.

DE Apoptosis regulator Bcl-2.

GN Name=BCL2;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN (1) \_TaxID=9606;

RP NUCLEOTIDE SEQUENCE (ISOFORMS ALPHA AND BETA).

RX MEDLINE=86259760; PubMed=3523487;

RA Tsujimoto Y., Croce C.M.;

RT "Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma.";

RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).

RN (2)

RP SEQUENCE REVISION TO 96; 110 AND 237.

RX MEDLINE=92375724; PubMed=1508712;

RA Eguchi Y., Ewert D.L., Tsujimoto Y.;

RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";

RL Nucleic Acids Res. 20:4187-4192(1992).

RN (3)

RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).

RX MEDLINE=87002488; PubMed=2875799; DOI=10.1016/0092-8674(86)90362-4;

RA Cleary M.L., Smith S.D., Sklar J.;

RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14;18) translocation.";

RL Cell 47:19-28(1986).

RN (4)

RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).

RX MEDLINE=88196071; PubMed=2834197;

RA Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,

RA Goldman P., Korsmeyer S.J.;

RT "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-Ig fusion gene in lymphoma.";

RL EMBO J. 7:123-131(1988).

RN (5)

RP NUCLEOTIDE SEQUENCE (GENOMIC DNA), AND VARIANT THR-43.

RN Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,

RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,

RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;

RT "NIH-SNPs, environmental genome project, NIH-SNPs ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

RN (6)

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA], AND VARIANT SER-7.  
RX MEDLINE=88217344; PubMed=3285301;  
RA Hua C., Zorn S., Jensen J.P., Coupland R.W., Ko H.S., Wright J.J.,  
RA Bakhshi A.;  
RT "Consequences of the t(14;18) chromosomal translocation in follicular  
RT lymphoma: deregulated expression of a chimeric and mutated Bcl-2  
RT gene";  
RL Oncogene Res. 2:263-275 (1988).  
RN [7]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).  
RC TISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulliahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [8]  
RP NUCLEOTIDE SEQUENCE OF 1-131 (ISOFORM ALPHA), AND VARIANTS NON-HODGKIN  
RP LYMPHOMA SER-59 AND ILE-93.  
RX MEDLINE=92096610; PubMed=1339299;  
RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;  
RT "Frequent incidence of somatic mutations in translocated BCL2  
RT oncogenes of non-Hodgkin's lymphomas";  
RL Blood 79:229-237 (1992).  
RN [9]  
RP SUBCELLULAR LOCATION  
RX MEDLINE=91066924; PubMed=2250705; DOI=10.1038/348334a0;  
RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;  
RT "Bcl-2 is an inner mitochondrial membrane protein that blocks  
RT programmed cell death.";  
RL Nature 348:334-336 (1990).  
RN [10]  
RP MUTAGENESIS.  
RX MEDLINE=94239528; PubMed=8183370; DOI=10.1038/369321a0;  
RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;  
RT "Bhl and BH2 domains of Bcl-2 are required for inhibition of apoptosis  
RT and heterodimerization with Bax";  
RL Nature 369:321-323 (1994).  
RN [11]  
RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.  
RX MEDLINE=98057466; PubMed=9395403; DOI=10.1126/science.278.5345.1966;  
RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,  
RA Ueno K., Hardwick J.M.;  
RT "Conversion of Bcl-2 to a Bax-like death effector by caspases";  
RL Science 278:1966-1968 (1997).  
RN [12]  
RP INTERACTION WITH TP53BP2.  
RX MEDLINE=96251339; PubMed=8668206;  
RA Naumovski L., Cleary M.L.;  
RT "The p53-binding protein 53BP2 also interacts with Bcl2 and impedes  
RT cell cycle progression at G2/M";  
RL Mol. Cell. Biol. 16:3884-3892 (1996).  
RN [13]  
RP REVIEW ON PHOSPHORYLATION.  
RX MEDLINE=21260650; PubMed=11368354; DOI=10.1038/sj/leu/2402090;  
RA Ruvoilo P.P., Deng X., May W.S.;  
RT "Phosphorylation of Bcl2 and regulation of apoptosis";  
Leukemia 15:515-522 (2001).  
[14]  
RP PHOSPHORYLATION BY ASK1/JNK1.  
RX MEDLINE=20036804; PubMed=10567572;  
RA Yamamoto K., Ichijo H., Korsmeyer S.J.;  
RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal  
RT protein kinase pathway normally activated at G(2)/M";  
RL Mol. Cell. Biol. 19:8469-8478 (1999).  
RN [15]  
RP INTERACTIONS WITH BBC3 AND BCL2L1.  
RX MEDLINE=21394643; PubMed=11463391; DOI=10.1016/S1097-2765(01)00213-1;  
RA Yu J., Zhang L., Huang P.M., Kinzler K.W., Vogelstein B.;  
RT "PUMA induces the rapid apoptosis of colorectal cancer cells";  
RL Mol. Cell 7:673-682 (2001).  
RN [16]  
RP INTERACTIONS WITH BNIP1.  
RX MEDLINE=22783925; PubMed=12901880; DOI=10.1016/S0006-291X(03)01387-1;  
RA Qin W., Hu J., Guo M., Xu J., Li J., Yao G., Zhou X., Jiang H.,  
RA Zhang P., Shen L., Wan D., Gu J.;  
RT "BNIP1-2, a novel homologue of BNIP-2, interacts with Bcl-2 and  
RT Cdc42GAP in apoptosis";  
RL Biochem. Biophys. Res. Commun. 308:379-385 (2003).  
CC -I- FUNCTION: Suppresses apoptosis in a variety of cell systems  
CC including factor-dependent lymphohematopoietic and neural cells.  
CC Regulates cell death by controlling the mitochondrial membrane  
CC permeability. Appears to function in a feedback loop system with  
CC caspases. Inhibits caspase activity either by preventing the  
CC release of cytochrome c from the mitochondria and/or by binding to  
CC the apoptosis-activating factor (APAF-1).  
CC -I- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
CC Bcl-X(L). Heterodimerization with BAX requires intact Bhl and BH2  
CC motifs, and is necessary for anti-apoptotic activity (By  
CC similarity). Also interacts with APAF-1, RAP-1, TP53BP2, BBC3,  
CC BCL2L1 and BNIP1.  
CC -I- INTERACTION:  
CC Self: NbExp=1; IntAct=EBI-77694, EBI-77694, EBI-77694;  
CC Q36P68-7; NbExp=1; IntAct=EBI-77694, EBI-519832;  
CC Q29294:BAD; NbExp=3; IntAct=EBI-77694, EBI-700771;  
CC Q61337:Bad (xeno); NbExp=2; IntAct=EBI-77694, EBI-400328;  
CC Q16611:BAK1; NbExp=1; IntAct=EBI-77694, EBI-519886;  
CC Q07812:BAX; NbExp=2; IntAct=EBI-77694, EBI-516580;  
CC Q07813:Bax (xeno); NbExp=1; IntAct=EBI-77694, EBI-700711;  
CC Q9BXH1:BBC3; NbExp=2; IntAct=EBI-77694, EBI-519884;  
CC Q9BXH1-1:BBC3; NbExp=1; IntAct=EBI-77694, EBI-519891;  
CC Q9BXH1-2:BBC3; NbExp=1; IntAct=EBI-77694, EBI-519896;  
CC P51572:BCAP31; NbExp=2; IntAct=EBI-77694, EBI-77683;  
CC O43521:BCL2L1; NbExp=1; IntAct=EBI-77694, EBI-526406;  
CC O43521-2:BCL2L1; NbExp=1; IntAct=EBI-77694, EBI-526420;  
CC O34918:Bcl2l1l1 (xeno); NbExp=1; IntAct=EBI-77694, EBI-526067;  
CC P55957:Bid; NbExp=2; IntAct=EBI-77694, EBI-519672;  
CC Q13323:Bik; NbExp=1; IntAct=EBI-77694, EBI-700794;  
CC Q91259:Bmf (xeno); NbExp=1; IntAct=EBI-77694, EBI-708032;  
CC -I- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
CC membrane of the nuclear envelope and the endoplasmic reticulum.  
CC -I- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Alpha;  
CC IsoId=P10415-1; Sequence=Displayed;  
CC Name=Beta;  
CC IsoId=P10415-2; Sequence=VSP\_000512;  
CC -I- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
CC -I- DOMAIN: The BH4 motif is required for anti-apoptotic activity and  
CC for interaction with RAP-1.  
CC -I- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
CC occurs during the G2/M phase of the cell cycle. In the absence of  
CC growth factors, Bcl2 appears to be phosphorylated by other protein  
CC kinases such as ERKs and stress-activated kinases.  
CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
CC PPM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleaved protein, lacking the BH4 motif, has pro-apoptotic  
CC activity, causes the release of cytochrome c into the cytosol

CC promoting further caspase activity.  
 CC -!- DISEASE: A chromosomal aberration involving BCL2 may be a cause of

Query Match 85.8%; Score 769.5; DB 1; Length 239;  
 Best Local Similarity 72.5%; Pred. No. 1.5e-64;  
 Matches 150; Conservative 2; Mismatches 14; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQSGYEWDAAGD-----DVENRTEAPE 45  
 DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQSGYEWDAAGDGAAPGAPAPGIESQPGHTPHDA 60

QY 46 GTE-----EVVHLALQAGDDFSRRYRGDFAEMSSQLH 79  
 DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPPVHLTLRQAGDDFSRRYRGDFAEMSSQLH 120

QY 80 LTPFTARGPATVVEELFRDGVNMGRIVAFFFGVCMVESVNREMSPLVDNIALWMTEY 139  
 DB 121 LTPFTARGPATVVEELFRDGVNMGRIVAFFFGVCMVESVNREMSPLVDNIALWMTEY 180

QY 140 LNRHLHTWIQDNGGDAFVELYGPMSR 166  
 DB 181 LNRHLHTWIQDNGGDAFVELYGPMSR 207

RESULT 2  
 BCL2 BOVIN STANDARD; PRT; 229 AA.

AC Q0278;  
 DT 26-SEP-2001, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JUL-1997, sequence version 1.  
 DT 07-MAR-2006, entry version 50.

DE Apoptosis regulator Bcl-2.  
 GN Name=BCL2;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 -OX NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RC STRAIN=Holstein; TISSUE=Thymus;  
 RX MEDLINE=98162580; PubMed=9501036; DOI=10.1006/viro.1998.9029;  
 RA Reyes R.A., Cockerell G.L.;  
 RT "Increased ratio of bcl-2/bax expression is associated with bovine  
 RT leukemia virus-induced leukemogenesis in cattle.";  
 RL Virology 242:184-192(1998).

CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1) (By similarity).

CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC motifs, and is necessary for anti-apoptotic activity. Also  
 CC interacts with APAF-1, RAF-1, TP53BP2, BIRC3, BCL2L1 and BNIP1 (By  
 CC similarity).

CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum (By  
 CC similarity).

CC -!- DOMAIN: The BH4 motif is required for anti-apoptotic activity and  
 CC for interaction with RAF-1 (By similarity).

CC -!- PTM: Phosphorylation/dephosphorylation on Ser-63 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-63 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle (By similarity). In  
 CC the absence of growth factors, Bcl2 appears to be phosphorylated  
 CC by other protein kinases such as ERKs and stress-activated  
 CC kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By  
 CC similarity).

CC -!- PTM: Proteolytically cleaved by the BH4 motif, has pro-apoptotic  
 CC cleaved protein, lacking the BH4 motif, has pro-apoptotic

CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity (By similarity).  
 CC -!- SIMILARITY: Belongs to the Bcl-2 family.

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----  
 CC EMBL: U92434; AAB53319.1; -, mRNA.  
 CC HSSP: P10415; 1GJH.  
 CC InterPro: IPR013278; Apopt reg Bcl2.  
 CC InterPro: IPR012238; Bcl2\_apopt\_reg.  
 CC InterPro: IPR000712; Bcl2\_BH.  
 CC InterPro: IPR003093; Bcl2\_BH4.  
 CC InterPro: IPR002475; Bcl2\_family.  
 CC InterPro: IPR004725; Bcl2\_reg.  
 CC Pfam: PF00452; Bcl-2; 1.  
 CC Pfam: PF02180; BH4; 1.  
 CC PIRSF: PIRSF00115; Bcl2 antiapop; 1.  
 CC PIRSF: PIRSF001714; Bcl2\_apop\_reg; 1.  
 CC PRINTS: PR01863; APOPREGBCL2.  
 CC PRINTS: PR01862; BCL2FAMILY.  
 CC SMART: SM00337; BCL; 1.  
 CC SMART: SM00265; BH4; 1.  
 CC TIGRFAMs: TIGR00865; bcl-2; 1.  
 CC PROSITE: PS0062; BCL2\_FAMILY; 1.  
 CC PROSITE: PS01080; BH1; 1.  
 CC PROSITE: PS01258; BH2; 1.  
 CC PROSITE: PS01259; BH3; 1.  
 CC PROSITE: PS01260; BH4\_1; 1.  
 CC PROSITE: PS0063; BH4\_2; 1.  
 CC KW Apoptosis; Endoplasmic reticulum; Membrane; Mitochondrion;  
 CC Nuclear protein; Phosphorylation; Transmembrane.  
 CC FT CHAIN 1 229 Apoptosis regulator Bcl-2.  
 CC /FTID=PRO\_0000143046.

FT TRANSMEM 202 223 Potential.  
 FT MOTIF 10 30 BH4.  
 FT MOTIF 83 97 BH3.  
 FT MOTIF 126 145 BH1.  
 FT MOTIF 177 192 BH2.  
 FT COMPIAS 64 68 Poly-Pro.  
 FT COMPIAS 69 72 Poly-Ala.  
 FT SITE 34 35 Cleavage (by caspases) (By similarity).  
 FT MOD\_RES 63 63 Phosphoserine (by PKC) (By similarity).  
 SQ SEQUENCE 229 AA; 25100 MW; AD1DD0AF98FF1D CRC64;

Query Match 85.6%; Score 767.5; DB 1; Length 229;  
 Best Local Similarity 76.1%; Pred. No. 2.3e-64;  
 Matches 150; Conservative 2; Mismatches 14; Indels 31; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQSGYEWDAAGD-----DVENRTEAPE 45  
 DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQSGYEWDAAGDGAAPGAPAPGILSSQPGRTAPS 60

QY 46 GTE-----SEVVHLALQAGDDFSRRYRGDFAEMSSQLHPTTARGRF 89  
 DB 61 RSPPPPPAAAAGAPAPSPVPPVHLTLRQAGDDFSRRYRGDFAEMSSQLHPTTARERF 120

QY 90 ATVVEELFRDGVNMGRIVAFFFGVCMVESVNREMSPLVDNIALWMTEYLNRLHTWIQ 149  
 DB 121 ATVVEELFRDGVNMGRIVAFFFGVCMVESVNREMSPLVDNIALWMTEYLNRLHTWIQ 180

QY 150 DNGGWDADFVELYGPMSR 166  
 DB 181 DNGGWDADFVELYGPMSR 197

RESULT 3  
 Q81008 FELCA  
 ID Q81008\_FELCA PRELIMINARY; PRT; 235 AA.  
 AC Q81008;  
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-MAR-2006, entry version 16.

```
DE Bcl-2 protein.
GN Name=Bcl-2;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15893350; DOI=10.1016/j.rvec.2005.03.001;
RA Sano J., Nagafuchi S., Yamazaki J., Oguma K., Kano R., Hasegawa A.;
RT "Effect of anticneoplastic drugs on the expression of Bcl-2 and Bcl-xL
RL genes in the feline T-cell leukemia cell line.";
Res. Vet. Sci. 79:197-201(2005).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB096611; BAC24136.1; -; mRNA.
DR HSSP; P10415; IGJH.
DR SMR; Q81008; 40-203.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR013278; Apop_reg_Bcl2.
DR InterPro; IPR012238; Bcl2_apop_reg.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2-reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR PIRSF; PIRSF00115; Bcl2 antiapop; 1.
DR PIRSF; PIRSF001714; Bcl2 apop_reg; 1.
DR PRINTS; PR01863; APOPREGBCL2.
DR PRINTS; PR01862; BCL2FAMILY.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS0063; BH4; 1.
DR PROSITE; PS0063; BH4; 1.
SQ SEQUENCE 235 AA; 25621 MW; 2320B57C96B64548 CRC64;

Query Match 85.5%; Score 766.5; DB 2; Length 235;
Best Local Similarity 73.4%; Pred No. 2,9e-64;
Matches 149; Conservative 3; Mismatches 14; Indels 37; Gaps 2;

QY 1 MAHAGRTGYDNRREIYKVIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
Db 1 MAHAGRTGYDNRREIYKVIHYELPQRYEWDAGDAGAAPGAAAPGIFSQPGRTTAPA 60
QY 46 GTE-----SEVHLALROAGDDFSRRYRGDFAEWSQLHLTPF 83
Db 61 RTSPPPPVPAPAAAAAGPALSPPVPVHLTLROAGDDFSRRYRDRDFAEWSQLHLTPF 120
QY 84 TARGFATVVEELPRDGVNNGRIVAFVFFGGVNCVSNRMSPLVDNIALWMTEYLNHR 143
Db 121 TARGFATVVEELFRDGVNNGRIVAFVFFGGVNCVSNRMSPLVDNIALWMTEYLNHR 180
QY 144 LHTWIQDNGGWDFAVELYGPSNR 166
Db 181 LHTWIQDNGGWDFAVELYGPSNQ 203

RESULT 4
BCL2 RAT STANDARD; PRT; 236 AA.
AC P49550; Q62837; Q64032;
DT 01-OCT-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 2.
DT 07-MAR-2006, entry version 47.
```

```
DE Apoptosis regulator Bcl-2.
GN Name=Bcl2; Synonyms=Bcl-2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX TISSUE=Brain;
MEDLINE=94193015; PubMed=8144041; DOI=10.1016/0378-1119(94)90561-4;
RA Sato T., Irie S., Krajewski S., Reed J.C.;
RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
RL Gene 140:291-292(1994).
CC [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX STRAIN=Sprague-Dawley; TISSUE=Ovary;
MEDLINE=95129487; PubMed=7828536; DOI=10.1210/en.136.1.232;
RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT cell apoptosis is associated with decreased bax and constitutive bcl-2
RT and bcl-xlong messenger ribonucleic acid levels.";
RL Endocrinology 136:232-241(1995).
CC [3]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 19-172.
RX MEDLINE=95059917; PubMed=7969891; DOI=10.1016/0306-4522(94)90069-8;
RA Castrén E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
RA Lindholm D.;
RT "bcl-2 messenger RNA is localized in neurons of the developing and
RT adult rat brain.";
RL Neuroscience 61:165-177(1994).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
CC motifs, and is necessary for anti-apoptotic activity. Also
CC interacts with APAF-1, RAF-1, TP53BP2, BGC3, BCL2L1 and BNIP1 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with
CC highest levels in reproductive tissues. In the adult brain,
CC expression is localized in mitral cells of the olfactory bulb,
CC granule and pyramidal neurons of hippocampus, pontine nuclei,
CC cerebellar granule neurons, and in ependymal cells. In prenatal
CC brain, expression is higher and localized in the neuroepithelium
CC and in the cortical plate.
CC -1- DOMAIN: The BH4 motif is required for anti-apoptotic activity and
CC for interaction with RAF-1 (By similarity).
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.
CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 motif, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity (By similarity).
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; L14680; AAA53662.1; -; mRNA.
DR EMBL; U34964; AAA77687.1; -; mRNA.
```

EMBL; S74122; -, NOT\_ANNOTATED\_CDS; mRNA.  
 DR PIR; I53744; I53744.  
 DR PIR; I67432; I67432.  
 DR HSSP; P10415; I67432.  
 DR SMR; P49950; 41-204.  
 DR Ensembl; ENSRNOG00000002791; Rattus norvegicus.  
 DR RGD; 2199; Bcl2.  
 DR GO; GO:0006916; P:anti-apoptosis; IDA.  
 DR GO; GO:0006915; P:apoptosis; TAS.  
 DR InterPro; IPR013278; Apoptosis; Bcl2.  
 DR InterPro; IPR012238; Bcl2\_apop\_reg.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR004725; Bcl2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR PIRSF; PIRSF00115; Bcl2\_antiapop; 1.  
 DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
 DR PRINTS; PR01863; APOREGCL2.  
 DR PRINTS; PR01862; BCL2FAMILY.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM0265; BH4; 1.  
 DR TIGRFS; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS0062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS0063; BH4\_2; 1.  
 DR Apoptosis; Endoplasmic reticulum; Membrane; Mitochondrion;  
 KW Nuclear protein; Phosphorylation; Transmembrane.  
 FT CHAIN 1 236 /ftid=PRO\_0000143050.  
 FT TRANSMEM 209 230 Potential.  
 FT MOTIF 10 30 BH4.  
 FT MOTIF 90 104 BH3.  
 FT MOTIF 133 152 BH1.  
 FT MOTIF 184 199 BH2.  
 FT SITE 34 35 Cleavage (by caspases) (By similarity).  
 FT MOD\_RES 70 70 Phosphoserine (by PKC) (By similarity).  
 FT CONFLICT 42 42 A -> R (in Ref. 2).  
 FT CONFLICT 157 157 E -> G (in Ref. 1).  
 FT CONFLICT 164 164 S -> Y (in Ref. 2).  
 FT CONFLICT 212 212 L -> Q (in Ref. 2).  
 SQ SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;  
 Query Match 85.4%; Score 766; DB 1; Length 236;  
 Best Local Similarity 73.5%; Pred. No. 3.3e-64;  
 Matches 150; Conservative 3; Mismatches 13; Indels 38; Gaps 2;  
 QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDD-----VEENRTEA 43  
 DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDD-----VEENRTEA 60  
 QY 44 PECTES-----EVVHLALROAGDDFRRYRGDAFSSQLHLTP 82  
 DB 61 VHRDTAARTSPRLPLVANAGPALSPVPPVHLTLRAGDDFRRYRGDAFSSQLHLTP 120  
 QY 83 FTARGRFATVVELFRDGVNMGRIIVAFRRFGGVMCVESVNRMSPLVDNIALWMTEYLNR 142  
 DB 121 FTARGRFATVVELFRDGVNMGRIIVAFRRFGGVMCVESVNRMSPLVDNIALWMTEYLNR 180  
 QY 143 HLHTWIQDNGWDADFVELYGPSMR 166  
 DB 181 HLHTWIQDNGWDADFVELYGPSMR 204  
 RESULT 5  
 ID Q75SV7 CANFA PRELIMINARY; PRT; 239 AA.  
 AC Q75SV7;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

05-JUL-2004, sequence version 1.  
 07-FEB-2006, entry version 11.  
 Name=bcl-2;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 OC Canis.  
 NCBI\_TaxID=9615;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sano J., Yamazaki J., Nagafuchi S., Kano R., Hasegawa A.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; AB154172; BAD05044.1; -; mRNA.  
 DR HSSP; P53563; IAF3.  
 DR SMR; Q75SV7; 44-207.  
 DR Ensembl; ENSCAFG00000000068; Canis familiaris.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR013278; Apop\_reg\_Bcl2.  
 DR InterPro; IPR012238; Bcl2\_apop\_reg.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR PIRSF; PIRSF00115; Bcl2\_antiapop; 1.  
 DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM0265; BH4; 1.  
 DR TIGRFS; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS0062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS0063; BH4\_2; 1.  
 SQ SEQUENCE 239 AA; 25923 MW; 74AE30048C875973 CRC64;  
 Query Match 85.3%; Score 765.5; DB 2; Length 239;  
 Best Local Similarity 72.0%; Pred. No. 3.7e-64;  
 Matches 149; Conservative 4; Mismatches 13; Indels 41; Gaps 2;  
 QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVENRTEAPE 45  
 DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVENRTEAPE 60  
 QY 46 GTE-----SEVHLALROAGDDFRRYRGDAFSSQLHLTP 79  
 DB 61 RTSPPPPPAPAAAAAADAAGAPSPVPPVHLTLRAGDDFRRYRGDAFSSQLHLTP 120  
 QY 80 LTPFTARGRFATVVELFRDGVNMGRIIVAFRRFGGVMCVESVNRMSPLVDNIALWMTEYL 139  
 DB 121 LTPFTARGRFATVVELFRDGVNMGRIIVAFRRFGGVMCVESVNRMSPLVDNIALWMTEYL 180  
 QY 140 LNRHLHTWIQDNGWDADFVELYGPSMR 166  
 DB 181 LNRHLHTWIQDNGWDADFVELYGPSMR 207  
 RESULT 6  
 ID Q4VBF6 MOUSE PRELIMINARY; PRT; 236 AA.  
 AC Q4VBF6;  
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE Bcl2 protein.

GN Name=Bcl2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Olfactory epithelium;  
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Alcega S.F., Zeeberg B., Bueow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Olfactory epithelium;  
RG NIH MGC Project;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBSJ databases.  
CC  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
DR EMBL; BC095964; AAH95964.1; -; mRNA.  
DR SMR; QAVB6; 41-204  
DR MGI; MGI:88138; Bcl2.  
DR GO; GO:0005829; Cytozol; IDA.  
DR GO; GO:0005739; C:mitochondrion; IDA.  
DR GO; GO:0005515; P:protein binding; IPT.  
DR GO; GO:0006916; P:anti-apoptosis; IGI.  
DR GO; GO:0006916; P:anti-apoptosis; IDA.  
DR GO; GO:0006916; P:apoptosis; IDA.  
DR GO; GO:0001836; P:release of cytochrome c from mitochondria; IDA.  
DR InterPro; IPR013278; Bcl2\_family.  
DR InterPro; IPR012238; Bcl2\_apop\_reg.  
DR InterPro; IPR000712; Bcl2\_BH4.  
DR InterPro; IPR003093; Bcl2\_family.  
DR InterPro; IPR002475; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS0063; BH4\_2; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS0063; BH4\_2; 1.  
SQ SEQUENCE 236 AA; 26407 MW; 80FDCFE78C735092 CRC64;

Query Match 84.4%; Score 757; DB 2; Length 236;

Best Local Similarity 72.2%; Pred. No. 2.3e-63;

Matches 151; Conservative 1; Mismatches 9; Indels 48; Gaps 3;

Qy 1 MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAAGDDVEENRTEAPEGT-----ES 49  
Db 1 MAQAGRTGYDNREIVMKYIHYKLSQRGYEWDAAGD-----ADAAPLGAAPTGGIFSFPES 55  
Qy 50 E-----VVHLALRQAGDDFSRRYRGDFAEWSSQ 77  
Db 56 NPMPAVHRDMAARTSPRLPLVATAGPALSPVPVPHLTLRAGDDFSRRYRRDFAEWSSQ 115  
Qy 78 LHLPFTTARGRTATVVEELFRDGVNMGRIVAFPEFGGVMCVESVNRMSPLVDNIALWMT 137  
Db 116 LHLPFTTARGRTATVVEELFRDGVNMGRIVAFPEFGGVMCVESVNRMSPLVDNIALWMT 175  
Qy 138 EYLNRLHHTWIDQNGGWDFAVELYGPMSMR 166  
Db 176 EYLNRLHHTWIDQNGGWDFAVELYGPMSMR 204  
RESULT 7  
Q7TSN8 RAT PRELIMINARY; PRT; 236 AA.  
ID Q7TSN8 RAT AC Q7TSN8; 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2003, sequence version 1.  
DT 07-FEB-2006, entry version 15.  
DE Bcl2-like protein.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Wistar;  
RA Tanaka T., Nangaku M.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.  
CC  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
DR EMBL; AF512835; AAP47159.1; -; mRNA.  
DR HSSP; P10415; 1GJH.  
DR SMR; Q7TSN8; 41-204.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR013278; Apop\_reg\_Bcl2.  
DR InterPro; IPR012238; Bcl2\_apop\_reg.  
DR InterPro; IPR000712; Bcl2\_BH4.  
DR InterPro; IPR003093; Bcl2\_family.  
DR InterPro; IPR002475; Bcl2\_reg.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR PIRSF; PIRSF00115; Bcl2\_antiapop; 1.  
DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS0063; BH4\_2; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
SQ SEQUENCE 236 AA; 26407 MW; 80FDCFE78C735092 CRC64;

Query Match 84.4%; Score 757; DB 2; Length 236;

Best Local Similarity 72.2%; Pred. No. 2.3e-63;

Matches 151; Conservative 1; Mismatches 9; Indels 48; Gaps 3;

Qy 1 MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAAGDDVEENRTEAPEGT-----ES 49  
Db 1 MAQAGRTGYDNREIVMKYIHYKLSQRGYEWDAAGD-----ADAAPLGAAPTGGIFSFPES 55

QY 50 E-----VVHLALRQAGDSSRRYRGDAFEMSSQ 77  
 Db 56 NMPFAVHRDMAARTSLPLRVATAGPALSVPVPPVHLTLRRAGDDFSRRYRDRFAEMSSQ 115  
 QY 78 LHLPPTPTARGTATVEELFRDGVNNGRIVAFEFVGVCVMSVNVNREMSPLVDNIALWMT 137  
 Db 116 LHLPPTPTARGTATVEELFRDGVNNGRIVAFEFVGVCVMSVNVNREMSPLVDNIALWMT 175  
 QY 138 EYLNRLHLTWIQDNGWMDAFVELYGFPSMR 166  
 Db 176 EYLNRLHLTWIQDNGWMDAFVELYGFPSMR 204  
 RESULT 8  
 Q8BOK4 MOUSE  
 ID Q8BOK4\_MOUSE PRELIMINARY; PRT; 236 AA.  
 AC Q8BOK4\_MOUSE  
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 22.  
 DE 7 days embryo whole body cDNA, RIKEN full-length enriched library,  
 DE clone:C430015F12 product:B-cell leukemia/lymphoma 2, full insert  
 DE sequence.  
 GN Name=Bcl2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Whole body; STRAIN=C57BL/6J;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Methods Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,  
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 RA Bansal K.P., Baxter L., Belsel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA Fletcher C.P., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
 RA Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakagawa H., Ng P.,  
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
 RA Petrosky N., Piazza S., Reid J.F., Ring J.P., Ring B.Z., Ringwald M.,  
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,  
 RA Tamaojo K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki K., Tomaru Y.,  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,

RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563(2005).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group  
 RG (Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense Transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566(2005).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Oatono N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konggaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RL 60,770 full-length cDNAs.";  
 RL Nature 402:563-573(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=21085860; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.







```
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -!- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AJ271720; CAB92245.1; -, mRNA.
CC PIR; JC7383; JC7383.
CC HSP; P10415; IGJH.
CC SMR; Q9JUV8; 41-204.
CC InterPro; IPR013278; Apop_reg_Bcl2.
CC InterPro; IPR012338; Bcl2_apop_reg.
CC InterPro; IPR000712; Bcl2_BH.
CC InterPro; IPR003093; Bcl2_BH4.
CC InterPro; IPR002475; Bcl2_family.
CC InterPro; IPR004725; Bcl2_reg.
CC Pfam; PF00452; Bcl-2; 1.
CC Pfam; PF02180; BH4; 1.
CC PIRSF; PIRSF00115; Bcl2_antiapop; 1.
CC PIRSF; PIRSF001714; Bcl2_apop_reg; 1.
CC PRINTS; PR01863; APOREGCL2.
CC PRINTS; PR01862; BCL2FAMILY.
CC SMART; SM00337; BCL; 1.
CC TIGRFAMs; TIGR00865; bcl-2; 1.
CC PROSITE; PS00662; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01259; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC PROSITE; PS01259; BH4; 1.
CC PROSITE; PS01260; BH4_1; 1.
CC PROSITE; PS00063; BH4_2; 1.
CC Apoptosis; Endoplasmic reticulum; Membrane; Mitochondrion;
CC Nuclear protein; Phosphorylation; Transmembrane. Bcl-2.
FT CHAIN 1 236 Apoptosis regulator Bcl-2.
FT FTID=PRO.0000143047.
FT TRANSMEM 209 230 Potential.
FT MOTIF 10 30 BH4.
FT MOTIF 90 104 BH3.
FT MOTIF 133 152 BH1.
FT MOTIF 184 199 BH2.
FT SITE 64 65 Cleavage (by caspase-3 and caspase-9).
FT MOD_RES 70 70 Phosphoserine (by PKC) (By similarity).
SQ SEQUENCE 236 AA; 26491 MW; BECADF1EF337228 CRC64;

Query Match 83.8%; Score 752; DB 1; Length 236;
Best Local Similarity 72.5%; Pred. No. 6.9e-63;
Matches 148; Conservative 2; Mismatches 16; Indels 38; Gaps 2;

QY 1 MAHAGRTGYDNRIVMKYIHYKLSQRYEWDAGD-----DVEENRTEA 43
DB 1 MAQAGRTGYDNRIVMKYIHYKLSQRYEWDGVDAAPIGAAPTGIQSFQESPTPA 60
QY 44 PE-----GTESEVVHLALROAGDDFSRRYRGDFAEKSSQLHLTP 82
DB 61 VHRDMAARTSPRLPVATTGPTLSPPVPPVHLLTRAGDDFSRRYRDFAEKSSQLHLTP 120
QY 83 FTARGFATVVEELFRDGVNMGRIIVAFEPFGVCMVESVNREMSPLVDNIALMTTYLNR 142
DB 121 FTARGFATVVEELFRDGVNMGRIIVAFEPFGVCMVESVNREMSPLVDNIALMTTYLNR 180
QY 143 HLHTWIQDNGGWDFAVELYGPSNR 166
DB 181 HLHTWIQDNGGWDFAVELYGPSVR 204

RESULT 10
BCL2_MOUSE STANDARD; PRT; 236 AA.
AC P10417; P10418;
DT 01-JUL-1989, integrated into UniProtKB/Swiss-Prot.
DT 01-APR-1993, sequence version 2.
DT 07-MAR-2006, entry version 63.
```

```
DE Apoptosis regulator Bcl-2.
GN Name=Bcl2; Synonyms=Bcl-2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX NUCLEOTIDE SEQUENCE [GENOMIC DNA] (ISOFORMS ALPHA AND BETA).
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=87187643; PubMed=302455; DOI=10.1016/0092-8674(87)90448-X;
RA Negri M., Silini E., Kozak C., Teujimoto Y.;
RT "Molecular analysis of mbcl-2: structure and expression of the murine
RL gene homologous to the human gene involved in follicular lymphoma.";
RN Cell 49:455-463(1987).
RX SEQUENCE REVISION TO 221-222.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Teujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RL in a variety of tissues including lymphoid and neuronal organs in
RN adult and embryo.";
RX Nucleic Acids Res. 20:4187-4192(1992).
RX PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.
RX MEDLINE=9727291; PubMed=9115213; DOI=10.1074/jbc.272.18.11671;
RA Ito T., Deng X., Carr B., May W.S. Jr.;
RT "Bcl-2 phosphorylation required for anti-apoptosis function.";
RN J. Biol. Chem. 272:11671-11673(1997).
RX DEPHOSPHORYLATION BY PP2A.
RX MEDLINE=99069407; PubMed=9852076; DOI=10.1074/jbc.273.51.34157;
RA Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;
RT "Reversible phosphorylation of Bcl2 following interleukin 3 or
RN bryostatine 1 is mediated by direct interaction with protein
RX phosphatase 2A*.";
RX J. Biol. Chem. 273:34157-34163(1998).
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1).
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
CC motifs, and is necessary for anti-apoptotic activity. Also
CC interacts with APAF-1, RAF-1, TP53BP2, BIRC3, BCL2L1 and BHIPL (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC ISOID=P10417-1; Sequence=Displayed;
CC Name=Beta;
CC ISOID=P10417-2; Sequence=VSP_000513;
CC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC -!- DOMAIN: The BH4 motif is required for anti-apoptotic activity and
CC for interaction with RAF-1.
CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.
CC Dephosphorylated by protein phosphatase 2A (PP2A).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 motif, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -!- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
```

```
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
DR EMBL; L31532; AAA37282.1; -; Genomic_DNA.
DR EMBL; M16506; AAA37282.1; JOINED; Genomic_DNA.
DR EMBL; M16506; AAA37281.1; -; Genomic_DNA.
DR PIR; B25960; TVMSB1.
DR HSSP; P10415; IGJH.
DR SMR; P10415; IGJH.
DR Ensembl; ENSMUSG00000057329; Mus musculus.
DR MGI; MGI:88138; Bcl2.
DR Reactome; P10417; -.
DR GO; GO:0005829; C:cytosol; IDA.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR GO; GO:000515; F:protein binding; IPI.
DR GO; GO:0006916; P:anti-apoptosis; IDA.
DR GO; GO:0006915; P:apoptosis; IDA.
DR GO; GO:0001836; P:release of cytochrome c from mitochondria; IDA.
DR InterPro; IPR013278; Apop_reg_Bcl2.
DR InterPro; IPR012238; Bcl2_apop_reg.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR PIRSF; PIRSF00115; Bcl2_antiapop; 1.
DR PIRSF; PIRSF001714; Bcl2_apop_reg; 1.
DR PRINTS; PR01863; APOPREGHCL2.
DR PRINTS; PR01862; BCL2_FAMILY.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRfam; TIGR00865; bcl-2; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS0063; BH4-2; 1.
DR MOD_RES; 70 70
DR VARSPIC; 193 236
KW Alternative splicing; Apoptosis; Endoplasmic reticulum; Membrane;
KW Mitochondrion; Nuclear protein; Phosphorylation; Transmembrane.
FT CHAIN 1 236
FT TRANSMEM 209 230
FT MOTIF 10 30
FT MOTIF 90 104
FT MOTIF 133 152
FT MOTIF 184 199
FT SITE 34 35
FT MOD_RES 70 70
FT VARSPIC 193 236
FT FT
FT FT
SQ SEQUENCE 236 AA; 26425 MW; AA85EP6E0766BE0A CRC64;

Query Match 83.8%; Score 752; DB 1; Length 236;
Best Local Similarity 71.8%; Pred. No. 6.9e-63;
Matches 150; Conservative 1; Mismatches 10; Indels 48; Gaps 3;

QY 1 MAHAGRTGYDNRREIWMKYIHYKLSQRGYEWDAAGDDVVENRTEAPGTT-----ES 49
DB 1 MAQAGRTGYDNRREIWMKYIHYKLSQRGYEWDAAGDDVVENRTEAPGTTGIFSFQFQES 55
QY 50 E-----VVHLALRQAGDDFRRYRGDFAEMSSQ 77
DB 56 NMPAVHREMAARTSPRLVATAGPALSPVPPCVHLTLRRAGDDFRRYRDRFAEMSSQ 115
QY 78 LHLTPFTARGFATVVEELFRDGVNMGRIVAFPEFGVNCVSVNREMSPLVDNIALMWT 137
DB 116 LHLTPFTARGFATVVEELFRDGVNMGRIVAFPEFGVNCVSVNREMSPLVDNIALMWT 175
QY 138 EYLNRLHTWTIQDNGGDAFVELYGPSMR 166
|||||
```

```
Db 176 EYLNRLHTWTIQDNGGDAFVELYGPSMR 204

RESULT 11
Q923R6 CRIOLO
ID Q923R6 CRIOLO PRELIMINARY; PRT; 236 AA.
AC Q923R6;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE B-cell lymphoma protein 2.
GN Name=bcl2;
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetidae; Cricetinae; Cricetus.
OX NCBI_TaxID=10030;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lai D.-Z., Chen W., Wang H.T.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF040339; AAK92201.1; -; mRNA.
DR HSSP; P10415; IGJH.
DR SMR; Q923R6; 41-204.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR013278; Apop_reg_Bcl2.
DR InterPro; IPR012238; Bcl2_apop_reg.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR PIRSF; PIRSF00115; Bcl2_antiapop; 1.
DR PIRSF; PIRSF001714; Bcl2_apop_reg; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRfam; TIGR00865; bcl-2; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS0063; BH4-2; 1.
DR SEQUENCE 236 AA; 26501 MW; BEDF052EF32CA8B8 CRC64;

Query Match 83.8%; Score 752; DB 2; Length 236;
Best Local Similarity 72.5%; Pred. No. 6.9e-63;
Matches 148; Conservative 2; Mismatches 16; Indels 38; Gaps 2;

QY 1 MAHAGRTGYDNRREIWMKYIHYKLSQRGYEWDAAGD-----DVENRTEA 43
DB 1 MAQAGRTGYDNRREIWMKYIHYKLSQRGYEWDAAGDAAAPLGAAPTGIFSFQFQESNPTPA 60
QY 44 PE-----GTESEVVHLALRQAGDDFRRYRGDFAEMSSQHLTP 82
DB 61 VHRDMAARTSPRLVATGTTLSPPVPVHLTLRRAGDDFRRYRDRFAEMSSQHLTP 120
QY 83 FTARGFATVVEELFRDGVNMGRIVAFPEFGVNCVSVNREMSPLVDNIALMWT EYLNRL 142
DB 121 FTARGFATVVEELFRDGVNMGRIVAFPEFGVNCVSVNREMSPLVDNIALMWT EYLNRL 180
QY 143 HLHTWTIQDNGGDAFVELYGPSMR 166
DB 181 HLHTWTIQDNGGDAFVELYGPSVR 204

RESULT 12
```

Q6R755 CANFA  
ID Q6R755 CANFA PRELIMINARY; PRT; 236 AA.  
AC Q6R755;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 11.  
DE Bcl-2.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
OC Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RA Chien M.B., London C.A., Jones C.S.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
CC EMBL; AY509563; AAR92491.1; -; mRNA.  
DR HSSP; P53563; 1AF3.  
DR SMR; Q6R755; 41-204.  
DR Ensembl; ENSCARG0000000068; Canis familiaris.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR013278; P:regulation of apoptosis; IEA.  
DR InterPro; IPR012238; Apop reg Bcl2.  
DR InterPro; IPR000712; Bcl2\_apop\_reg.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2 family.  
DR InterPro; IPR004725; BCL2 reg.  
DR Pfam; PF02180; BH4; 1.  
DR Pfam; PF00452; Bcl-2; 1.  
DR PIRSF; PIRSF500115; Bcl2 antiapop; 1.  
DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRfams; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2 FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 236 AA; 26449 MW; BC22E0CEFD3EB228 CRC64;  
  
Query Match 83.5%; Score 749; DB 2; Length 236;  
Best Local Similarity 72.1%; Pred. No. 1.3e-62;  
Matches 147; Conservative 3; Mismatches 16; Indels 38; Gaps 2;  
  
QY 1 MAHAGTGYDNRREIVMKYHYKLSQRYEWDAGD-----DVEENRTEA 43  
DB 1 MAAGTGYDNRREIVMKYHYKLSQRYEWDGVDAAFLGAAPTFGIFSFQESNPTPA 60  
QY 44 PE-----GTESEVHLALRQAGDDFSRRYRGDFAEMSSQLHLTP 82  
DB 61 VHRDMAARTSPLRPIVATTGPTLSPPVPVHLTLRAGDDFSRRYRDFAEMSSQLHLTP 120  
QY 83 FTARGSFATVVEELFRDGVNWRGRIVAFFFGVCMVESVNREMSPLVDNIALMTTEYLNR 142  
DB 121 FTARGSFATVVEELFRDGVNWRGRIVAFFFGVCMVESVNREMSPLVDNIALMTTEYLNR 180  
QY 143 HLHTWIQDNGGWDFAVELYGPSMR 166  
DB 181 HLHTWIQDNGGWDFAVELYGPSMTQ 204  
  
RESULT 13  
Q8MJ81 BOVIN  
ID Q8MJ81 BOVIN PRELIMINARY; PRT; 185 AA.  
AC Q8MJ81;  
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2002, sequence version 1.  
DT 07-FEB-2006, entry version 13.  
DE Bcl2 protein (Fragment).  
GN Name=bcl2;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=Jersey;  
RC MEDLINE=22542224; PubMed=12655025; DOI=10.1093/nar/gng037;  
RA Krebs S., Medugorac I., Seichter D., Forster M.;  
RT "RNaseCut: a MALDI mass spectrometry-based method for SNP discovery.";  
RL Nucleic Acids Res. 31:E37-E37(2003).  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
CC EMBL; AF515848; AAN03862.1; -; Genomic\_DNA.  
DR HSSP; P10415; 1GJH.  
DR Ensembl; ENSBTAG00000019302; Bos taurus.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR013278; Apop reg Bcl2.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2 family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS50062; BCL2 FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
DR NON\_TER 185 185  
FT SEQUENCE 185 AA; 20260 MW; 8FA829629553C65F CRC64;  
  
Query Match 79.4%; Score 712.5; DB 2; Length 185;  
Best Local Similarity 75.1%; Pred. No. 2.9e-59;  
Matches 139; Conservative 2; Mismatches 13; Indels 31; Gaps 2;  
  
QY 1 MAHAGTGYDNRREIVMKYHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
DB 1 MAAGTGYDNRREIVMKYHYKLSQRYEWDAGAGAAPGAPGILSOFGRTPAPS 60  
QY 46 GTE-----SEVHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGRF 89  
DB 61 RTSPPPPPAAAAGPAPSPVPVPHVHLTLRQAGDDFSRRYRDFAEMSSQLHLTPFTARGRF 120  
QY 90 ATTVVEELFRDGVNWRGRIVAFFFGVCMVESVNREMSPLVDNIALMTTEYLNRHLHTWIQ 149  
DB 121 ATTVVEELFRDGVNWRGRIVAFFFGVCMVESVNREMSPLVDNIALMTTEYLNRHLHTWIQ 180  
QY 150 DNGGW 154  
DB 181 DNGGW 185  
  
RESULT 14  
BCL2 CHICK  
ID BCL2 CHICK STANDARD; PRT; 233 AA.  
AC Q00709;  
DT 01-APR-1993, integrated into UniProtKB/Swiss-Prot.  
DT 01-APR-1993, sequence version 1.  
DT 07-MAR-2006, entry version 45.  
DE Apoptosis regulator Bcl-2.  
GN Name=BCL2; Synonyms=BCL-2;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA MEDLINE=92375724; PubMed=1508712;  
RX Equchi Y., Ewert D.L., Teujimoto Y.;  
RA "Isolation and characterization of the chicken bcl-2 gene: expression  
RT in a variety of tissues including lymphoid and neuronal organs in  
RT adult and embryo.";  
RL Nucleic Acids Res. 20:4187-4192(1992).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=B-cell lymphoma;  
RX MEDLINE=92379084; PubMed=1511008; DOI=10.1016/0167-4781(92)90064-7;  
RA Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;  
RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken  
RT homologue of the Bcl-2 oncoprotein.";  
RL Biochim. Biophys. Acta 1132:109-113 (1992).  
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems  
CC including factor-dependent lymphohematopoietic and neural cells.  
CC Regulates cell death by controlling the mitochondrial membrane  
CC permeability. Appears to function in a feedback loop system with  
CC caspases. Inhibits caspase activity either by preventing the  
CC release of cytochrome c from the mitochondria and/or by binding to  
CC the apoptosis-activating factor (APAF-1).  
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2  
CC motifs, and is necessary for anti-apoptotic activity (By  
CC similarity). Also interacts with APAF-1 and RAF-1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
CC membrane of the nuclear envelope and the endoplasmic reticulum.  
CC -!- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,  
CC kidney, heart, ovary and brain, with the highest levels in the  
CC thymus. In the embryo, highly levels expressed in all tissues with  
CC high levels in the bursa of Fabricius.  
CC -!- DOMAIN: The BH4 motif is required for anti-apoptotic activity and  
CC for interaction with RAF-1 (By similarity).  
CC -!- SIMILARITY: Belongs to the Bcl-2 family.  
CC  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
CC -----  
DR EMBL; D11382; BAA01978.1; -; Genomic\_DNA.  
DR EMBL; Z11961; CAA78018.1; -; mRNA.  
DR PIR; A37332; A37332.  
DR PIR; S24390; S24390.  
DR HSSP; P10415; 1G5M.  
DR SMR; Q00709; 38-201.  
DR Ensembl; ENSGALG00000012885; Gallus gallus.  
DR InterPro; IPR013278; Apop\_reg Bcl2.  
DR InterPro; IPR012238; Bcl2\_apop\_reg.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR PIRSF; PIRSF001115; Bcl2 antiapop; 1.  
DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
DR PRINTS; PR01863; APOPRE5BCL2.  
DR PRINTS; PR01862; BCL2FAMILY.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH2; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4; 1.  
DR PROSITE; PS0063; BH4\_2; 1.  
KW Apoptosis; Endoplasmic reticulum; Membrane; Mitochondrion;  
KW Nuclear protein; Transmembrane.  
FT CHAIN 1 233 Apoptosis regulator Bcl-2.

FT TRANSMEM 208 228  
FT MOTIF 10 30  
FT MOTIF 87 101  
FT MOTIF 130 149  
FT MOTIF 181 196  
FT CONFLICT 64 64  
FT CONFLICT 67 82  
FT CONFLICT 121 121  
FT CONFLICT 139 139  
SQ SEQUENCE 233 AA; 25687 MW; 52525555ACB6E4C3D CRC64;  
  
Query Match 79.2%; Score 710.5; DB 1; Length 233;  
Best Local Similarity 69.2%; Pred. No. 5.9e-59;  
Matches 139; Conservative 7; Mismatches 20; Indels 35; Gaps 3;  
  
QY 1 MAHAGRTGYDNREIVMKYIHYKLSQRYEWDAGDD-----VEE 38  
DB 1 MAHPGRGYDNREIVLKYIHYKLSQRYDWAAGEDRPVPAPAPAAAPAAAGASSH 60  
QY 39 NRTEAP-EGTSEV-----VHLALROAGDDFSRRYRGDFPAEMSSQLHLPFTA 85  
DB 61 HRPEPPGSAASAEVPPAEGLRPAPPVGHVHLALROAGDEFSRRYORDFQAQMSQLHLPFTA 120  
QY 86 RGRFATVVEELFRDGVNMGRIVAFFERFGVCMVESVNNREMSPLVDNIALMTVEYLNRLHL 145  
DB 121 HGRFVAVVEELFRDGVNMGRIVAFFERFGVCMVESVNNREMSPLVDNIALMTVEYLNRLHL 180  
QY 146 TWIQDNGGWDFAVELYGPSMR 166  
DB 181 NWIQDNGGWDFAVELYGNMSR 201  
  
RESULT 15  
Q6NTH7\_MOUSE  
ID Q6NTH7\_MOUSE PRELIMINARY; PRT; 199 AA.  
AC Q6NTH7;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 13.  
DE B-cell leukemia/lymphoma 2.  
GN Name=Bcl2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus gland;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus gland;  
 RA Strausberg R.;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 CC  
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC  
 CC EMBL; BC068988; AAH68988.1; -; mRNA.  
 DR HSSP; P53563; IAF3.  
 DR SMR; Q6NTH7; 41-192.  
 DR Ensembl; ENSMUSG00000057329; Mus musculus.  
 DR MGI; MGI:88138; Bcl2.

GO; GO:0005829; C:cytosol; IDA.  
 GO; GO:0005739; C:mitochondrion; IDA.  
 GO; GO:0005515; F:protein binding; IPI.  
 GO; GO:0006916; P:anti-apoptosis; IGI.  
 GO; GO:0006916; P:anti-apoptosis; IDA.  
 GO; GO:0006915; P:apoptosis; IDA.  
 GO; GO:0001836; P:release of cytochrome c from mitochondria; IDA.  
 DR InterPro; IPR013278; Apop reg Bcl2.  
 DR InterPro; IPR012238; Bcl2\_apop\_reg.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR PROSITE; PSS0062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; UNKNOWN\_1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4\_1; 1.  
 DR PROSITE; PSS0063; BH4\_2; 1.  
 DR PROSITE; PSS0063; BH4\_2; 1.  
 SQ SEQUENCE 199 AA; 22281 MW; F13C8037262BA955 CRC64;

Query Match 77.4%; Score 694; DB 2; Length 199;  
 Best Local Similarity 70.6%; Pred. No. 1.8e-57;  
 Matches 139; Conservative 1; Mismatches 9; Indels 48; Gaps 3;  
 QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDDVEENRTEAECT-----ES 49  
 DB 1 MAQAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----ADAAPLGAATPGIFSFPES 55  
 QY 50 E-----VHIALRQAGDDFSRRYRGDFAEISSQ 77  
 DB 56 NMPAVHRDMAARTSLRPLVATAGPALSPVPVHVHLLRRAGDDFSRRYRDFAEISSQ 115  
 QY 78 LHLTPFTARGFATVVEELFRDGVNWRGRIVAFPEFGVNCVESVNRMSPLVDNIALWMT 137  
 DB 116 LHLTPFTARGFATVVEELFRDGVNWRGRIVAFPEFGVNCVESVNRMSPLVDNIALWMT 175  
 QY 138 EYLNRLHLTWIQDNGGW 154  
 DB 176 EYLNRLHLTWIQDNGGW 192

Search completed: December 30, 2006, 12:12:39  
 Job time : 303 secs

This Page Blank (uspto,

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2006, 12:07:51 ; Search time 39 Seconds  
(without alignments)  
409.538 Million cell updates/sec

Title: US-09-716-395-2  
Perfect score: 897  
Sequence: 1 MAHAGRTGYDNRIVMKYIH.....WIQDNGWDFAVELYGPSMR 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	769.5	85.8	239	1 TVHUA1	transforming prote
2	760	84.7	236	2 I67432	BCL-2 - rat (fragm
3	759	84.6	236	2 I53744	gene bcl-2 protein
4	752	83.8	236	1 TVMSA1	transforming prote
5	752	83.8	236	2 JC7383	B-cell lymphoma 2
6	718.5	80.1	205	1 TVHUB1	transforming prote
7	710.5	79.2	233	2 A37332	transforming prote
8	689	76.8	199	1 TVMSB1	transforming prote
9	689	76.8	232	2 S24390	transforming prote
10	656.5	73.2	216	2 B37332	transforming prote
11	527	57.8	233	2 B47537	apoptosis regulato
12	511	57.0	233	2 I49056	bcl-x long - mouse
13	505	56.3	233	2 S51761	BCL-X protein - ra
14	494	55.1	214	2 I49057	bcl-x transmembran
15	489	54.5	227	2 JE0203	apoptosis regulato
16	489	54.5	233	2 I67431	BCL-X-Long - rat
17	486	54.2	154	2 I58194	gene bcl-2 protein
18	415	46.3	190	2 A47537	apoptosis regulato
19	219	24.4	170	2 I49055	bcl-x short - mous
20	213	23.7	176	2 I67435	gene bcl-xshort pr
21	175	19.5	211	2 S58873	Bak protein - huma
22	173	19.3	211	2 S58875	cdn-2 protein - hu
23	172.5	19.2	133	2 I53295	bcl-2-associat
24	172	19.2	192	2 I47538	bcl-2-associat p
25	161	17.9	192	2 A47538	bcl-2-associat p
26	155.5	17.3	175	2 I39055	Bcl-2 related - hu
27	148.5	16.6	143	2 I38921	bcl-2-associat p
28	148	16.5	179	2 JC7255	Bax-delta protein
29	146.5	16.3	218	2 B47538	bcl-2-associat p

BCL2 homolog MCL1  
hemopoietic-specif  
NR-13 protein - qu  
Mcl-1a protein - z  
protein ced-9 (imp  
apoptosis suppress  
cytochrome P450 1A  
response regulator  
electron transfer  
HsdR type IC restr  
beta-galactosidase  
probable membrane  
dolichyl-phosphate  
hypothetical prote  
hypothetical prote  
probable prolyl en

ALIGNMENTS

RESULT 1

TVHUA1

transforming protein bcl-2, splice form alpha - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1988 #sequence revision 07-Jun-1996 #text change 05-Oct-2004

C;Accession: C37332; A29409; S02452; A24428; A27622; B27622

R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari-

A;Reference number: A37332; MUID:92375724; PMID:1508712

A;Accession: C37332

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-239 <EGU>

A;Cross-references: UNIPROT:PI0415; UNIPARC:UPI000000D90E

A;Note: this report is a correction

R;Tsujimoto, Y.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

A;Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gen-

A;Reference number: A29409; MUID:86259760; PMID:3523487

A;Accession: A29409

A;Molecule type: mRNA

A;Residues: 1-95, 'A', 'G', '111-236, 'S', '238-239 <TSU>

A;Cross-references: UNIPARC:UPI000002F8D7; GB:M13994; NID:G179366; PIDN:AAA51813.1; PID

A;Note: this sequence has been corrected in reference A37332

R;Seto, M.; Jaeger, U.; Hockett, R.D.; Granger, W.; Bennett, S.; Goldman, P.; Korsmeyer

EMBO J. 7, 123-131, 1988

A;Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-

A;Reference number: S02452; MUID:88196071; PMID:2834197

A;Accession: S02452

A;Molecule type: mRNA

A;Residues: 1-239 <SET>

A;Cross-references: UNIPARC:UPI000000D90E

R;Cleary, M.L.; Smith, S.D.; Sklar, J.

Cell 47, 19-28, 1986

A;Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunogl

A;Reference number: A24428; MUID:87002488; PMID:2875799

A;Accession: A24428

A;Molecule type: mRNA

A;Residues: 1-58, 'T', '60-116, 'R', '118-239 <CLE>

A;Cross-references: UNIPARC:UPI0000035C80; GB:M14745; NID:G179370; PIDN:AAA35591.1; PID

R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A.

Oncogene Res. 2, 263-275, 1988

A;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:

A;Reference number: A27622; MUID:88217344; PMID:3285301

A;Accession: A27622

A;Molecule type: mRNA

A;Residues: 1-58, 'T', '60-239 <HUA>

A;Cross-references: UNIPARC:UPI00000173303

A;Accession: B27622

A;Molecule type: DNA

A;Residues: 1-6, 'S', '8-58, 'T', '60-128, 'C', '130-239 <HUA2>



A;Cross-references: UNIPARC:UPI0000173303  
A;Note: the sequence was determined from the germline gene  
C;Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation  
C;Genetics:  
A;Gene: GDB:BCL2  
A;Cross-references: GDB:119031; OMIM:151430  
A;Map position: 18q21.3-18q21.3  
C;Function:  
A;Description: blocks apoptosis in hematopoietic cells  
C;Superfamily: Bcl2 related apoptosis regulator  
C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto  
Query Match 85.8%; Score 769.5; DB 1; Length 239;  
Best Local Similarity 72.5%; Pred. No. 1.1e-66;  
Matches 150; Conservative 2; Mismatches 14; Indels 41; Gaps 2;  
Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGD-----DVENRTEA 45  
Db 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGDVGAAAPGAPGIFSSQPGHTHPA 60  
Qy 46 GTES-----EVHLALRQAGDDFSRRYRGDFAEMSSQLH 79  
Db 61 ASRDPVARTSPLOTPAAPCAAGPALSPVPVVLTLRQAGDDFSRRYRRDFAEMSSQLH 120  
Qy 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 139  
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 180  
Qy 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166  
Db 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207  
RESULT 2  
IG7432  
BCL-2 - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Oct-2004  
C;Accession: IG7432  
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equiva  
onstitutive bcl-2 and bcl-xiong messenger ribonucleic acid levels.  
A;Reference number: 153295; MUID:95129487; PMID:7828536  
A;Accession: IG7432  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-236 <RES>  
A;Cross-references: UNIPROT:P49950; UNIPARC:UPI00001707FF; EMBL:U34964; NID:G1004378; PI  
C;Superfamily: Bcl2 related apoptosis regulator

Query Match 84.7%; Score 760; DB 2; Length 236;  
Best Local Similarity 73.0%; Pred. No. 8.8e-66;  
Matches 149; Conservative 3; Mismatches 14; Indels 38; Gaps 2;  
Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGD-----VVENRTEA 43  
Db 1 MAQAGRTGYDNREIVMKYIHVKLSQRYEWDGDSAPLRAPTPGIFSFQPSNRTPA 60  
Qy 44 PEGTES-----EVHLALRQAGDDFSRRYRGDFAEMSSQLH 82  
Db 61 VHRDTAARTSPLRPLVANAGPALSPVPVVLTLRAGDDFSRRYRRDFAEMSSQLH 120  
Qy 83 FTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 142  
Db 121 FTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 180  
Qy 143 HLHTWIQDNGWDADFVELYGPMSR 166  
Db 181 HLHTWIQDNGWDADFVELYGPMSR 204  
RESULT 3  
IG7432  
BCL-2 - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Oct-2004  
C;Accession: IG7432  
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equiva  
onstitutive bcl-2 and bcl-xiong messenger ribonucleic acid levels.  
A;Reference number: 153295; MUID:95129487; PMID:7828536  
A;Accession: IG7432  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-236 <RES>  
A;Cross-references: UNIPROT:P49950; UNIPARC:UPI00001707FF; EMBL:U34964; NID:G1004378; PI  
C;Superfamily: Bcl2 related apoptosis regulator

153744  
Gene bcl-2 protein - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 05-Oct-2004  
C;Accession: I53744  
R;Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.  
Gene 140, 291-292, 1994  
A;Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.  
A;Reference number: I53744; MUID:94193015; PMID:8144041  
A;Accession: I53744  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-236 <RES>  
A;Cross-references: UNIPROT:P49950; UNIPARC:UPI000014728C; GB:L14680; NID:G408946; PIDN:  
C;Genetics:  
A;Gene: bcl-2  
C;Superfamily: Bcl2 related apoptosis regulator  
Query Match 84.6%; Score 759; DB 2; Length 236;  
Best Local Similarity 73.0%; Pred. No. 1.1e-65;  
Matches 149; Conservative 3; Mismatches 14; Indels 38; Gaps 2;  
Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGD-----VVENRTEA 43  
Db 1 MAQAGRTGYDNREIVMKYIHVKLSQRYEWDGDSAPLRAPTPGIFSFQPSNRTPA 60  
Qy 44 PEGTES-----EVHLALRQAGDDFSRRYRGDFAEMSSQLH 82  
Db 61 VHRDTAARTSPLRPLVANAGPALSPVPVVLTLRAGDDFSRRYRRDFAEMSSQLH 120  
Qy 83 FTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 142  
Db 121 FTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 180  
Qy 143 HLHTWIQDNGWDADFVELYGPMSR 166  
Db 181 HLHTWIQDNGWDADFVELYGPMSR 204  
RESULT 4  
TWMSA1  
transforming protein bcl-2-alpha - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 05-Oct-2004  
C;Accession: A25960; E37332  
R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.  
Cell 49, 455-463, 1987  
A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homol  
A;Reference number: A90893; MUID:87187643; PMID:3032455  
A;Accession: A25960  
A;Molecule type: DNA  
A;Residues: 1-236 <NEG>  
A;Cross-references: UNIPARC:UPI00001470CA; GB:L31532; GB:M16506; NID:G468336; PIDN:AAA37  
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie  
A;Reference number: A37332; MUID:92375724; PMID:1508712  
A;Accession: E37332  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A;Molecule type: DNA  
A;Residues: 1-33,'E',34-220,'AL',223-236 <EGU>  
A;Cross-references: UNIPARC:UPI0000173306  
C;Genetics:  
A;Gene: BCL2  
C;Superfamily: Bcl2 related apoptosis regulator  
C;Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro  
Query Match 83.8%; Score 752; DB 1; Length 236;  
Best Local Similarity 71.8%; Pred. No. 5.2e-65;  
Matches 150; Conservative 1; Mismatches 10; Indels 48; Gaps 3;  
Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGD-----VVENRTEA 43  
ES 49

```
Db 1 MAQAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----ADAAPLGAAPTGGIFSFQPS 55
Qy 50 E-----VVHLALROAGDDFSRRYRGDFAEQSSQ 77
Db 56 NMPAVHREMAARTSPRLVATAGPALSPVPPVHLTLRRAGDDFSRRYRRDFAEQSSQ 115
Qy 78 LHLTPFTARGFATVVEELFRDGVNMGRIVAFFFGVCMVESVNREMSPLVDNIALMWT 137
Db 116 LHLTPFTARGFATVVEELFRDGVNMGRIVAFFFGVCMVESVNREMSPLVDNIALMWT 175
Qy 138 EYLNRLHLHTWIQDNGWDFAVELYGPSMR 166
Db 176 EYLNRLHLHTWIQDNGWDFAVELYGPSMR 204

RESULT 5
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C:Species: Cricetus griseus (Chinese hamster)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 05-Oct-2004
C:Accession: JC7383
R:Tomicic, M.T.; Christmann, M.; Kaina, B.
Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A:Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A:Reference number: JC7383
A:Contents: Ovary
A:Accession: JC7383
A:Molecule type: mRNA
A:Residues: 1-236 <TOM>
A:CROSS-references: UNIPROT:Q9JJV8; UNIPARC:UPI0000126829; GB:AJ271720
C:Comment: This protein has anti-apoptotic function, and supports cell survival.
C:Genetics:
A:Gene: bcl-2
C:Superfamily: Bcl2 related apoptosis regulator
C:Keywords: B-cell lymphoma; ovary

Query Match 83.8%; Score 752; DB 2; Length 236;
Best Local Similarity 72.5%; Pred. No. 5.2e-65;
Matches 148; Conservative 2; Mismatches 16; Indels 38; Gaps 2;

Qy 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEA 43
Db 1 MAQAGRTGYDNRREIVMKYIHYKLSQRYEWDVDAAPLGAAPTGGIFSFQPSNPTPA 60
Qy 44 PE-----GTESEVHLALROAGDDFSRRYRGDFAEQSSQLHLTP 82
Db 61 VHRDMAARTSPRLPIVATTGPTLSPPVPPVHLTLRRAGDDFSRRYRRDFAEQSSQLHLTP 120
Qy 83 FTARGFATVVEELFRDGVNMGRIVAFFFGVCMVESVNREMSPLVDNIALMWT EYLN 142
Db 121 FTARGFATVVEELFRDGVNMGRIVAFFFGVCMVESVNREMSPLVDNIALMWT EYLN 180
Qy 143 HLHTWIQDNGWDFAVELYGPSMR 166
Db 181 HLHTWIQDNGWDFAVELYGPSVR 204

RESULT 6
TVHUB1
Transforming protein bcl-2, splice form beta - human
N:Alternate names: apoptosis regulator bcl-2
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004
R:Tsujimoto, Y.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene
A:Reference number: A29409; MUID:86259760; PMID:3523487
A:Accession: B29409
A:Molecule type: mRNA
A:Residues: 1-205 <TSU>
A:CROSS-references: UNIPROT:P10415; UNIPARC:UPI0000043C0D; GB:M13995; NID:gl79368; PIDN:
```

```
R:Tanaka, S.; Louie, D.C.; Kant, J.A.; Reed, J.C.
Blood 79, 229-237, 1992
A:Title: Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-I
A:Reference number: I52566; MUID:92096610; PMID:1339299
A:Accession: I52566
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-131 <TAN>
A:CROSS-references: UNIPARC:UPI000016B445; GB:S72602; NID:G241046; PIDN:AAD14111.1; PID
R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari
A:Reference number: A37332; MUID:92375724; PMID:1508712
A:Accession: D37332
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-33, 'E', '34-95, 'T', '97-109, 'R', '111-205 <EGU>
A:CROSS-references: UNIPARC:UPI0000173305
C:Genetics:
A:Gene: GDB:BCL2
A:CROSS-references: GDB:119031; OMIM:151430
A:Map position: 18q21.3-18q21.3
C:Function:
A:Description: blocks apoptosis in hematopoietic cells
C:Superfamily: Bcl2 related apoptosis regulator
C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proce

Query Match 80.1%; Score 718.5; DB 1; Length 205;
Best Local Similarity 71.8%; Pred. No. 7.4e-62;
Matches 140; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

Qy 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAPGIFSSQGHPTHPA 60
Qy 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEQSSQLH 79
Db 61 ASRDPVARTSPLOTPAAPAAAGPALSPVPPVHLALROAGDDFSRRYRGDFAEQSSQLH 120
Qy 80 LTPFTARGFATVVEELFRDGVNMGRIVAFFFGVCMVESVNREMSPLVDNIALMWT EY 139
Db 121 LTPFTARGFATVVEELFRDGVNMGRIVAFFFGVCMVESVNREMSPLVDNIALMWT EY 180
Qy 140 LNRHLHTWIQDNGW 154
Db 181 LNRHLHTWIQDNGW 195

RESULT 7
A37332
Transforming protein (bcl-2-alpha) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Oct-2004
C:Accession: A37332; S35453
R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari
A:Reference number: A37332; MUID:92375724; PMID:1508712
A:Accession: A37332
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-233 <EGU>
A:CROSS-references: UNIPROT:Q00709; UNIPARC:UPI0000126828; EMBL:D11381
C:Genetics:
A:Introns: 189/3
C:Superfamily: Bcl2 related apoptosis regulator
C:Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 79.2%; Score 710.5; DB 2; Length 233;
Best Local Similarity 69.2%; Pred. No. 5.1e-61;
Matches 139; Conservative 7; Mismatches 20; Indels 35; Gaps 3;

Qy 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
```

```
||||| 1 MAHGRRTGYDNREIVLKYIHYKLSQRYGVDWAAGSDRPVPPAPAPAAAPAAVAAAGASSH 60
39 NRTEAP-EGTSEV-----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
61 HRPEPPGSAASEVPPAEGLRPAPPGVHLALRQAGDEFSSRYQRDFQMSQQLHLTPFTA 120
86 RGRFATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 145
121 HGRFVAVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 180
146 TWIQDNGWDAPVELYGPSMR 166
181 NWIQDNGWDAPVELYGNMSR 201

RESULT 8
TWMS31
transforming protein bcl-2-beta - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004
C:Accession: B25960
R:Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homol
A:Reference number: A90893; MUID:87187643; PMID:3032455
A:Accession: B25960
A:Molecule type: DNA
A:Residues: 1-199 <NEG>
A:Cross-references: UNIPROT:P10417; UNIPARC:UPI000002A4C2; GB:M16506; NID:g468335; PIDN:
C:Genetics:
C:Superfamily: Bcl2 related apoptosis regulator
C:Keywords: alternative splicing; transforming protein

Query Match 76.8%; Score 689; DB 1; Length 199;
Best Local Similarity 70.1%; Pred. No. 5e-59;
Matches 138; Conservative 1; Mismatches 10; Indels 48; Gaps 3;

Qy 1 MAHAGRTGYDNREIVMVKYIHYKLSQRYGVDWAAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Db 1 MAHAGRTGYDNREIVLKYIHYKLSQRYGVDWAAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Qy 39 NRTEAP-EGTSEV-----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Db 39 NRTEAP-EGTSEV-----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Qy 61 HRPEPPGSAASEVPPAEGLRPAPPGVHLALRQAGDEFSSRYQRDFQMSQQLHLTPFTA 120
Db 61 HRPEPPGSAASEVPPAEGLRPAPPGVHLALRQAGDEFSSRYQRDFQMSQQLHLTPFTA 120
Qy 86 RGRFATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 145
Db 86 RGRFATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 145
Qy 121 HGRFVAVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 180
Db 121 HGRFVAVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 180
Qy 146 TWIQDNGWDAPVELYGPSMR 166
Db 146 TWIQDNGWDAPVELYGPSMR 166
Qy 181 NWIQDNGWDAPVELYGNMSR 201
Db 181 NWIQDNGWDAPVELYGNMSR 201

RESULT 9
S24390
transforming protein (Bcl-2) homolog - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C:Accession: S24390
R:Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
Biochim. Biophys. Acta 1132, 109-113, 1992
A:Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue
A:Reference number: S24390; MUID:92379084; PMID:1511008
A:Accession: S24390
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-232 <CAZ>
A:Cross-references: UNIPROT:Q00709; UNIPARC:UPI000017124D; EMBL:Z11961; NID:g62969; PIDN
C:Superfamily: Bcl2 related apoptosis regulator
C:Keywords: mitochondrion; transmembrane protein
```

```
Query Match 76.8%; Score 689; DB 2; Length 232;
Best Local Similarity 66.3%; Pred. No. 6e-59;
Matches 136; Conservative 7; Mismatches 18; Indels 44; Gaps 3;

Qy 1 MAHAGRTGYDNREIVMVKYIHYKLSQRYGVDWAAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Db 1 MAHAGRTGYDNREIVLKYIHYKLSQRYGVDWAAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Qy 39 NRTEAP-EGTSEV-----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Db 39 NRTEAP-EGTSEV-----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Qy 61 HRPEPPGSAASEVPPAEGLRPAPPGVHLALRQAGDEFSSRYQRDFQMSQQLHLTPFTA 120
Db 61 HRPEPPGSAASEVPPAEGLRPAPPGVHLALRQAGDEFSSRYQRDFQMSQQLHLTPFTA 120
Qy 86 RGRFATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 145
Db 86 RGRFATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 145
Qy 121 HGRFVAVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 180
Db 121 HGRFVAVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 180
Qy 146 TWIQDNGWDAPVELYGPSMR 166
Db 146 TWIQDNGWDAPVELYGPSMR 166
Qy 176 RHLNWIQDNGWDAPVELYGNMSR 200
Db 176 RHLNWIQDNGWDAPVELYGNMSR 200

RESULT 10
B37332
transforming protein (bcl-2-beta) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Oct-2004
C:Accession: B37332; S35452
R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A:Reference number: A37332; MUID:92375724; PMID:1508712
A:Cross-references: UNIPARC:UPI0000176495; EMBL:D11381; EMBL:D11382
A:Superfamily: Bcl2 related apoptosis regulator
A:Molecule type: DNA
A:Residues: 1-216 <EGU>
A:Cross-references: UNIPARC:UPI0000176495; EMBL:D11381; EMBL:D11382
C:Superfamily: Bcl2 related apoptosis regulator

Query Match 73.2%; Score 656.5; DB 2; Length 216;
Best Local Similarity 67.7%; Pred. No. 7.5e-56;
Matches 128; Conservative 7; Mismatches 19; Indels 35; Gaps 3;

Qy 1 MAHAGRTGYDNREIVMVKYIHYKLSQRYGVDWAAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Db 1 MAHAGRTGYDNREIVLKYIHYKLSQRYGVDWAAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Qy 39 NRTEAP-EGTSEV-----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Db 39 NRTEAP-EGTSEV-----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Qy 61 HRPEPPGSAASEVPPAEGLRPAPPGVHLALRQAGDEFSSRYQRDFQMSQQLHLTPFTA 120
Db 61 HRPEPPGSAASEVPPAEGLRPAPPGVHLALRQAGDEFSSRYQRDFQMSQQLHLTPFTA 120
Qy 86 RGRFATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 145
Db 86 RGRFATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 145
Qy 121 HGRFVAVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 180
Db 121 HGRFVAVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 180
Qy 146 TWIQDNGWDAPVELYGPSMR 166
Db 146 TWIQDNGWDAPVELYGPSMR 166
Qy 176 RHLNWIQDNGWDAPVELYGNMSR 200
Db 176 RHLNWIQDNGWDAPVELYGNMSR 200
```

```
Query Match 73.2%; Score 656.5; DB 2; Length 216;
Best Local Similarity 67.7%; Pred. No. 7.5e-56;
Matches 128; Conservative 7; Mismatches 19; Indels 35; Gaps 3;

Qy 1 MAHAGRTGYDNREIVMVKYIHYKLSQRYGVDWAAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Db 1 MAHAGRTGYDNREIVLKYIHYKLSQRYGVDWAAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Qy 39 NRTEAP-EGTSEV-----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Db 39 NRTEAP-EGTSEV-----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTA 85
Qy 61 HRPEPPGSAASEVPPAEGLRPAPPGVHLALRQAGDEFSSRYQRDFQMSQQLHLTPFTA 120
Db 61 HRPEPPGSAASEVPPAEGLRPAPPGVHLALRQAGDEFSSRYQRDFQMSQQLHLTPFTA 120
Qy 86 RGRFATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 145
Db 86 RGRFATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 145
Qy 121 HGRFVAVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 180
Db 121 HGRFVAVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLHL 180
Qy 146 TWIQDNGWDAPVELYGPSMR 166
Db 146 TWIQDNGWDAPVELYGPSMR 166
Qy 176 RHLNWIQDNGWDAPVELYGNMSR 200
Db 176 RHLNWIQDNGWDAPVELYGNMSR 200

RESULT 11
B47537
apoptosis regulator bcl-xL - human
A:Alternate names: bcl-2-related protein
N:Contains: apoptosis regulator bcl-xs
C:Species: Homo sapiens (man)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Oct-2004
C:Accession: B47537; C47537
R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A:Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A:Reference number: A47537; MUID:93364977; PMID:8358789
A:Accession: B47537
```

A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-233 <BO1>  
A:Cross-references: UNIPROT:Q07817; UNIPARC:UPI000014624E; GB:L20121; NID:g510900; PIDN:  
F1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>  
F1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>  
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-69, 'G', 71-125,189-233 <BO2>  
A:Cross-references: UNIPARC:UPI00002A4C4; GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:  
C:Genetics:  
A:Gene: GDB:BCL2L  
A:Cross-references: GDB:228079  
C:Superfamily: Bcl2 related apoptosis regulator  
C:Keywords: alternative splicing; apoptosis  
F1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>  
F1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>  
Query Match 58.8%; Score 527; DB 2; Length 233;  
Best Local Similarity 53.1%; Pred. No. 2.5e-43;  
Matches 102; Conservative 17; Mismatches 33; Indels 40; Gaps 1;  
QY 11 NREIVMKYIHYKLSQKGYEWDAGDDVEENRTEAPECTESEV----- 51  
DB 5 NRELVDVFLSYKLSQKGYEWDAGDDVEENRTEAPECTESEMETPSPAINGNPSWHLADSPA 64  
QY 52 -----VHLALRQAGDDPSRRYRGDFAEKSSQLHLTPPTARGRFA 90  
DB 65 VNGATGCHSSSLDAREVPMAAVKQALREAGDFELRYRAFSDLTSQLHITPGTAYQSFE 124  
QY 91 TVVEELFRDGVNMGRIVAFPEFGVGVNREMSPLVDNIALWMTEYLNRLHHTWIOD 150  
DB 125 QVNNELFRDGVNMGRIVAFPEFGGALCVESVDKEMQVLSRIAAMWATYLNHLEPWIOE 184  
QY 151 NGGWDADFVELYG 162  
DB 185 NGGWDTFVDLYG 196  
RESULT 12  
I49056  
bcl-x long - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Oct-2004  
C:Accession: I49056; S52866  
R;Pang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A;Reference number: I49055; MUID:95052604; PMID:7963517  
A:Accession: I49056  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-233 <RES>  
A:Cross-references: UNIPARC:UPI000002103C; EMBL:U10101; NID:g506647; PIDN:  
R;Kamesaki, H.; Michaud, G.Y.; Takatou, K.; Okuma, M.  
submitted to the EMBL Data Library, November 1994  
A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line through  
A;Reference number: S52866  
A;Status: preliminary  
A:Accession: S52866  
A;Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-233 <KAM>  
A:Cross-references: UNIPARC:UPI000002103C; EMBL:X83574; NID:g955622; PIDN:CAA58557.1; PID:  
C:Superfamily: Bcl2 related apoptosis regulator  
Query Match 57.0%; Score 511; DB 2; Length 233;  
Best Local Similarity 51.6%; Pred. No. 8.7e-42;  
Matches 99; Conservative 18; Mismatches 35; Indels 40; Gaps 1;  
QY 11 NREIVMKYIHYKLSQKGYEWDAGDDVEENRTEAPECTESE----- 50  
DB 5 NRELVDVFLSYKLSQKGYEWDAGDDVEENRTEAPECTESEMETPSPAINGNPSWHLADSPA 64  
QY 51 -----VHLALRQAGDDPSRRYRGDFAEKSSQLHLTPPTARGRFA 90

DB 65 VNGATGCHSSSLDAREVPMAAVKQALREAGDFELRYRAFSDLTSQLHITPGTAYQSFE 124  
QY 91 TVVEELFRDGVNMGRIVAFPEFGVGVNREMSPLVDNIALWMTEYLNRLHHTWIOD 150  
DB 125 QVNNELFRDGVNMGRIVAFPEFGGALCVESVDKEMQVLSRIAAMWATYLNHLEPWIOE 184  
QY 151 NGGWDADFVELYG 162  
DB 185 NGGWDTFVDLYG 196  
RESULT 13  
I49057  
BCL-X protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 05-Oct-2004  
C:Accession: S51761; S51762  
R;Michaelidis, T.M.  
submitted to the EMBL Data Library, November 1994  
A;Reference number: S51761  
A:Accession: S51761  
A;Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-233 <MIC>  
A:Cross-references: UNIPROT:P53563; UNIPARC:UPI00001708BC; EMBL:X82537; NID:g607176; PIDN:  
A:Experimental source: embryonic; brain  
A:Accession: S51762  
A;Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-125,189-233 <M12>  
A:Cross-references: UNIPARC:UPI00001708BD; EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:  
A:Experimental source: embryonic; brain  
A;Note: smaller form due to splicing  
C:Genetics:  
A:Introns: 125/3  
C:Superfamily: Bcl2 related apoptosis regulator  
Query Match 56.3%; Score 505; DB 2; Length 233;  
Best Local Similarity 51.0%; Pred. No. 3.3e-41;  
Matches 98; Conservative 18; Mismatches 36; Indels 40; Gaps 1;  
QY 11 NREIVMKYIHYKLSQKGYEWDAGDDVEENRTEAPECTESE----- 50  
DB 5 NQELVVDVFLSYKLSQKGYEWDAGDDVEENRTEAPECTESEMETPSPAINGNPSWHLADSPA 64  
QY 51 -----VHLALRQAGDDPSRRYRGDFAEKSSQLHLTPPTARGRFA 90  
DB 65 VNGATGCHSSSLDAREVPMAAVKQALREAGDFELRYRAFSDLTSQLHITPGTAYQSFE 124  
QY 91 TVVEELFRDGVNMGRIVAFPEFGVGVNREMSPLVDNIALWMTEYLNRLHHTWIOD 150  
DB 125 QVNNELFRDGVNMGRIVAFPEFGGALCVESVDKEMQVLSRIAAMWATYLNHLEPWIOE 184  
QY 151 NGGWDADFVELYG 162  
DB 185 NGGWDTFVDLYG 196  
RESULT 14  
I49057  
bcl-x transmembrane deleted - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Oct-2004  
C:Accession: I49057  
R;Pang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A;Reference number: I49055; MUID:95052604; PMID:7963517  
A:Accession: I49057  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-214 <RES>



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: December 30, 2006, 12:26:47 ; Search time 44 Seconds  
(without alignments)  
369.134 Million cell updates/sec  
Title: US-09-716-395-2  
Perfect score: 897  
Sequence: 1 MAHAGRTGYDNRREIVNMYKH.....WTDNGGWDFAVELYGPSNR 166  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 390055 seqs, 97842647 residues  
Total number of hits satisfying chosen parameters: 390055  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New.\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	771.5	86.0	239	7	US-11-187-863-4
2	763.5	85.1	239	6	US-10-549-711-8
3	763.5	85.1	239	7	US-11-009-357-8
4	757.5	84.4	239	7	US-11-021-541-1705
5	757.5	84.4	236	7	US-11-021-541-1707
6	718.5	80.1	205	6	US-10-549-711-10
7	528	58.9	247	6	US-10-540-898-743
8	527	58.8	233	6	US-10-533-519-1168
9	527	58.8	233	6	US-10-533-519-1688
10	527	58.8	233	7	US-11-009-357-7
11	527	58.8	233	7	US-11-296-725-2
12	527	58.8	233	7	US-11-371-354-59735
13	527	58.8	233	7	US-11-021-541-1709
14	512	57.1	340	6	US-10-540-898-740
15	377.5	42.1	193	7	US-11-301-951-2
16	376.5	42.0	193	7	US-11-301-951-4
17	368.5	41.9	193	7	US-11-301-951-6
18	375.5	41.1	193	7	US-11-301-951-8
19	232	25.9	170	7	US-11-021-541-1721
20	175	19.5	211	7	US-11-371-354-72633
21	175	19.5	211	7	US-11-021-541-1715
22	174	19.4	192	7	US-11-021-541-1719
23	174	19.4	192	7	US-11-158-863-2
24	171.5	19.1	211	6	US-10-538-002-95
25	161	17.9	191	7	US-11-415-342-46

ALIGNMENTS

RESULT 1

US-11-187-863-4  
; Sequence 4, Application US/11187863  
; Publication No. US20060110793A1  
; GENERAL INFORMATION:  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: QU, ZHENGXING  
; APPLICANT: HORAK, EVA  
; APPLICANT: HORAK, IVAN D.  
; APPLICANT: CHANG, CHIEN HSING  
; APPLICANT: ROSSI, EDMOND A.  
; APPLICANT: YANG, JENG-DAR  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING LONGEVITY AND  
; TITLE OF INVENTION: PROTEIN YIELD FROM A CELL CULTURE  
; FILE REFERENCE: 40923-0194US1  
; CURRENT APPLICATION NUMBER: US/11/187,863  
; CURRENT FILING DATE: 2005-07-25  
; PRIOR APPLICATION NUMBER: 60/590,349  
; PRIOR FILING DATE: 2004-07-23  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 4  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: protein  
US-11-187-863-4

Query Match 86.0%; Score 771.5; DB 7; Length 239;  
Best Local Similarity 73.4%; Pred. No. 4.3e-74;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;  
QY 1 MAHAGRTGYDNRREIVNMYKHYSQRGYEWDAAGD-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 34  
DB 1 MAHAGRTGYDNRREIVNMYKHYSQRGYEWDAAGDVGAAAPGAAPGAPGIFSSQPGHTPHPA 60  
QY 35 -----DVEENRTEAPCTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVAREEPLQTAAAPGAAAGPALEPPVPHLTLROAGDDFSRRYRRDRFAEMSSQLH 120  
QY 80 LTPFTARGFAATVVEELFRDGVNNGRIVAFFEFGGVMCVESVNNREMSPLVDNIALWMTEY 139  
DB 121 LTPFTARGFAATVVEELFRDGVNNGRIVAFFEFGGVMCVESVNNREMSPLVDNIALWMTEY 180  
QY 140 LNRHLHTWTQDNGGWDFAVELYGPSNR 166  
|||||

Sequence 2, Appli  
Sequence 58719, A  
Sequence 1717, Ap  
Sequence 3000, Ap  
Sequence 1071, Ap  
Sequence 55127, A  
Sequence 123, App  
Sequence 6, Appli  
Sequence 27, Appli  
Sequence 4, Appli  
Sequence 18, Appli  
Sequence 5817, Ap  
Sequence 210, App  
Sequence 6583, Ap  
Sequence 9928, Ap  
Sequence 9927, Ap  
Sequence 9926, Ap  
Sequence 65929, A  
Sequence 1864, Ap  
US-10-550-280-2  
US-11-371-354-58719  
US-11-021-541-1717  
US-10-511-937-3000  
US-10-533-519-1071  
US-11-371-354-55127  
US-10-533-519-123  
US-10-550-280-6  
US-10-550-280-4  
US-11-409-944-27  
US-11-265-532A-4  
US-11-259-640A-18  
US-10-805-394-5817  
US-11-357-421-210  
US-10-805-394-6583  
US-10-953-349-9928  
US-10-953-349-9927  
US-10-953-349-9926  
US-11-371-354-65929  
US-10-526-324-1864

```
Db      181 LNRHLHTWIQDNGWDADFVLYGFSMR 207

RESULT 2
US-10-549-711-8
; Sequence 8, Application US/10549711
; Publication No. US20060223768A1
; GENERAL INFORMATION:
; APPLICANT: Milner, Josephine
; TITLE OF INVENTION: Regulation of Gene Expression
; FILE REFERENCE: 4100-0001
; CURRENT APPLICATION NUMBER: US/10/549,711
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: GB 0306148.8
; PRIOR FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-549-711-8

Query Match      85.1%; Score 763.5; DB 6; Length 239;
Best Local Similarity 72.5%; Pred. No. 3e-73;
Matches 150; Conservative 2; Mismatches 14; Indels 41; Gaps 2;

Qy      1 MAHAGRTGYDNRREIVMKYIHVYKLSQRYEWDAGD----- 34
Db      1 MAHAGRTGYDNRREIVMKYIHVYKLSQRYEWDAGDVGAAAPGAAAPAGPAGFFSQPGHTPTA 60

Qy      35 -----DVEENRTEAPGTS-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db      61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPVHLLTQAGDDFSRRYRRDFAEMSRQLH 120

Qy      80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 139
Db      121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 180

Qy      140 LNRHLHTWIQDNGWDADFVLYGFSMR 166
Db      181 LNRHLHTWIQDNGWDADFVLYGFSMR 207

RESULT 3
US-11-009-357-8
; Sequence 8, Application US/11009357
; Publication No. US20060127376A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Ute
; TITLE OF INVENTION: Methods and Compositions for Modulating Apoptotic Pathways
; FILE REFERENCE: STONYB-09615
; CURRENT APPLICATION NUMBER: US/11/009,357
; CURRENT FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-357-8

Query Match      85.1%; Score 763.5; DB 7; Length 239;
Best Local Similarity 72.5%; Pred. No. 3e-73;
Matches 150; Conservative 2; Mismatches 14; Indels 41; Gaps 2;

Qy      1 MAHAGRTGYDNRREIVMKYIHVYKLSQRYEWDAGD----- 34
Db      1 MAHAGRTGYDNRREIVMKYIHVYKLSQRYEWDAGDVGAAAPGAAAPAGPAGFFSQPGHTPTA 60

Qy      35 -----DVEENRTEAPGTS-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db      61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPVHLLTQAGDDFSRRYRRDFAEMSRQLH 120

Qy      80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 139
Db      121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 180

Qy      140 LNRHLHTWIQDNGWDADFVLYGFSMR 166
Db      181 LNRHLHTWIQDNGWDADFVLYGFSMR 207

RESULT 4
US-11-021-541-1705
; Sequence 1705, Application US/11021541
; Publication No. US20060287259A1
; GENERAL INFORMATION:
; APPLICANT: REICH, SAMUEL JOTHAM
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE
; FILE REFERENCE: DER-04-1324R
; CURRENT APPLICATION NUMBER: US/11/021,541
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,099
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 1733
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1705
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-541-1705

Query Match      84.4%; Score 757.5; DB 7; Length 239;
Best Local Similarity 71.5%; Pred. No. 1.3e-72;
Matches 148; Conservative 3; Mismatches 15; Indels 41; Gaps 2;

Qy      1 MAHAGRTGYDNRREIVMKYIHVYKLSQRYEWDAGD-----DVEENRTEAPE 45
Db      1 MAHAGRTGYDNRREIVMKYIHVYKLSQRYEWDAGDVGAAAPGAAAPAGPAGFFSQPGHTPTA 60

Qy      46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db      61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPVHLLTQAGDDFSRRYRRDFAEMSSQLH 120

Qy      80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 139
Db      121 LTPFTARGCFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 180

Qy      140 LNRHLHTWIQDNGWDADFVLYGFSMR 166
Db      181 LNRHLHTWIQDNGWDADFVLYGFSMR 207

RESULT 5
US-11-021-541-1707
; Sequence 1707, Application US/11021541
; Publication No. US20060287259A1
; GENERAL INFORMATION:
; APPLICANT: REICH, SAMUEL JOTHAM
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE
; FILE REFERENCE: DER-04-1324R
; CURRENT APPLICATION NUMBER: US/11/021,541
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,099
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 1733
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1707
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-021-541-1707
```



Query Match 84.4%; Score 757; DB 7; Length 236;  
Best Local Similarity 72.2%; Pred. No. 1.5e-72;  
Matches 151; Conservative 1; Mismatches 9; Indels 48; Gaps 3;  
QY 1 MAHAGTGYDNRREIVMKYIHYKLSQSGYEWDAAGDDVEENRTAPECT-----RS 49  
DB 1 MAQAGRTGYDNRREIVMKYIHYKLSQSGYEWDAAGD-----ADAAPLGAAPTGGIFSPQPS 55  
QY 50 E-----VHLALRQAGDDFRRYRGDFAFEMSSQ 77  
DB 56 NMPAVHRDMAARTSLPLVATAGPALSPVPVHLTLRRAGDDFRRYRGDFAFEMSSQ 115  
QY 78 LHLTPPTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVSVNREMSPLVDNIALMWT 137  
DB 116 LHLTPPTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVSVNREMSPLVDNIALMWT 175  
QY 138 EYLNRLHHTWIQDNGWDFAVELYGPMSR 166  
DB 176 EYLNRLHHTWIQDNGWDFAVELYGPMSR 204  
RESULT 6  
US-10-549-711-10  
; Sequence 10, Application US/10549711  
; Publication No. US20060223768A1  
; GENERAL INFORMATION:  
; APPLICANT: Milner, Josephine  
; TITLE OF INVENTION: Regulation of Gene Expression  
; FILE REFERENCE: 4100-0001  
; CURRENT APPLICATION NUMBER: US/10/549,711  
; PRIOR FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: GB 0306148.8  
; PRIOR FILING DATE: 2003-03-18  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 205  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-549-711-10

Query Match 80.1%; Score 718.5; DB 6; Length 205;  
Best Local Similarity 71.8%; Pred. No. 1.5e-68;  
Matches 140; Conservative 2; Mismatches 12; Indels 41; Gaps 2;  
QY 1 MAHAGTGYDNRREIVMKYIHYKLSQSGYEWDAAGD-----DVEENRTAPE 45  
DB 1 MAHAGTGYDNRREIVMKYIHYKLSQSGYEWDAAGDVGAAAPGGAAPGIFSPQGHPPHA 60  
QY 46 GTES-----EVHLALRQAGDDFRRYRGDFAFEMSSQLH 79  
DB 61 ASRDVPARTSPLOTPAAPGAAGPALSPVPVHLALRQAGDDFRRYRGDFAFEMSSQLH 120  
QY 80 LTPPTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVSVNREMSPLVDNIALMWT 139  
DB 121 LTPPTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVSVNREMSPLVDNIALMWT 180  
QY 140 LNRHLHTWIQDNGW 154  
DB 181 LNRHLHTWIQDNGW 195  
RESULT 7  
US-10-540-898-743  
; Sequence 743, Application US/10540898  
; Publication No. US20060166213A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: CHIR0056-101 (PPO23367.0003)  
; CURRENT APPLICATION NUMBER: US/10/540,898  
; CURRENT FILING DATE: 2005-06-27

; PRIOR APPLICATION NUMBER: US 10/330,773  
; PRIOR FILING DATE: 2002-12-27  
; NUMBER OF SEQ ID NOS: 981  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 743  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-540-898-743  
Query Match 58.9%; Score 528; DB 6; Length 247;  
Best Local Similarity 53.7%; Pred. No. 3.4e-48;  
Matches 102; Conservative 17; Mismatches 33; Indels 38; Gaps 1;  
QY 11 NREIVMKYIHYKLSQSGYEWDAAGDDVEENRTAPECTSEV----- 51  
DB 21 NRELVDVFLSYKLSQKGYSWQSOFSDVEENRTAPECTSEMPSEMSAINGNPSWHLADSPAVN 80  
QY 52 -----VHLALRQAGDDFRRYRGDFAFEMSSQLHLPFTTARGRFA 90  
DB 81 GATCHSSSLDAREVPMMAVKQALREAGDFELRYRRAFSDLTSQLHITPGTAYQSFQV 140  
QY 93 VEELFRDGVNMGRIIVAFEFEGGVMCVSVNREMSPLVDNIALMWTYLNRLHHTWIQDNG 152  
DB 141 VNELFRDGVNMGRIIVAFEFEGGALCVESVDKEMQVLVSRIAAAMATYLNHLEPWIQENG 200  
QY 153 GMDAFVELYG 162  
DB 201 GMDTFVELYG 210  
RESULT 8  
US-10-533-519-1168  
; Sequence 1168, Application US/10533519  
; Publication No. US20060263774A1  
; GENERAL INFORMATION:  
; APPLICANT: CLARK, HILARY  
; APPLICANT: SCHOENFELD, JILL  
; APPLICANT: VANLOOKEREN, MENNO  
; APPLICANT: WILLIAMS, P. MICKEY  
; APPLICANT: WOOD, WILLIAM I.  
; APPLICANT: WU, THOMAS D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE  
; TITLE OF INVENTION: RELATED DISEASES  
; FILE REFERENCE: P1984R1 US  
; CURRENT APPLICATION NUMBER: US/10/533,519  
; PRIOR FILING DATE: 2005-04-28  
; PRIOR APPLICATION NUMBER: PCT/US03/34312  
; PRIOR FILING DATE: 2003-10-30  
; PRIOR APPLICATION NUMBER: US 60/423,394  
; PRIOR FILING DATE: 2002-11-01  
; NUMBER OF SEQ ID NOS: 2517  
; SEQ ID NO 1168  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-533-519-1168  
Query Match 58.8%; Score 527; DB 6; Length 233;  
Best Local Similarity 53.1%; Pred. No. 4e-48;  
Matches 102; Conservative 17; Mismatches 33; Indels 40; Gaps 1;  
QY 11 NREIVMKYIHYKLSQSGYEWDAAGDDVEENRTAPECTSEV----- 51  
DB 5 NRELVDVFLSYKLSQKGYSWQSOFSDVEENRTAPECTSEMPSEMSAINGNPSWHLADSPA 64  
QY 52 -----VHLALRQAGDDFRRYRGDFAFEMSSQLHLPFTTARGRFA 90  
DB 65 VNGATCHSSSLDAREVPMMAVKQALREAGDFELRYRRAFSDLTSQLHITPGTAYQSF 124  
QY 91 TVVEELFRDGVNMGRIIVAFEFEGGVMCVSVNREMSPLVDNIALMWTYLNRLHHTWIQD 150  
DB 125 QVNNELFRDGVNMGRIIVAFEFEGGALCVESVDKEMQVLVSRIAAAMATYLNHLEPWIOE 184



```
FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59735
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-59735

Query Match      58.8%; Score 527; DB 7; Length 233;
Best Local Similarity 53.1%; Pred. No. 4e-48;
Matches 102; Conservative 17; Mismatches 33; Indels 40; Gaps 1;

QY 11 NREIVMKYIHYKLSQRYGWDAGDDVEENRTAPEGTESEV-----51
Db 5 NRELVDVFLSYKLSQKGYWSQFSDVEENRTAPEGTESEMETPSPAINGNPSWHLADSPA 64
QY 52 -----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGRA 90
Db 65 VNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPTAYQSP 124
QY 91 TVVEELFRDGVNNGRIVAFPEFGVVMCVESVNRMSPLVDNIALMWTYLNRLHHTWIOD 150
Db 125 QVVNELFRDGVNNGRIVAFPEFGGALCVESVDKEMQVLSRIAANWATYLNHLEPWIOE 184
QY 151 NGGWDAFVELYG 162
Db 185 NGGWDTFVELYG 196

RESULT 14
US-10-540-898-740
; Sequence 740, Application US/10540898
; Publication No. US20060166213A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0056-101 (PP023367.0003)
; CURRENT APPLICATION NUMBER: US/10/540,898
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 10/330,773
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 740
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-540-898-740

Query Match      57.1%; Score 512; DB 6; Length 340;
Best Local Similarity 50.8%; Pred. No. 2.6e-46;
Matches 100; Conservative 18; Mismatches 39; Indels 40; Gaps 1;

QY 6 RTGYNRELVMKYIHYKLSQRYGWDAGDDVEENRTAPEGTESE-----50
Db 92 RADPSNRELVDVFLSYKLSQKGYWSQFSDVEENRTAPEGTESEAINGNPSWHL 151
QY 51 -----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPETA 85
Db 152 ADSPAINGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPTGTA 211
QY 86 RGRFATVVEELFRDGVNNGRIVAFPEFGVVMCVESVNRMSPLVDNIALMWTYLNRLH 145
Db 212 YQSFQVNVNELFRDGVNNGRIVAFPEFGGALCVESVDKEMQVLSRIAANWATYLNH 271
QY 146 TWIQNGWDADFVELYG 162
Db 272 PWIQNGGWDTFVELYG 288

RESULT 15
US-11-301-951-2
; Sequence 2, Application US/11301951
; Publication No. US20060090214A1
; GENERAL INFORMATION:
; APPLICANT: Cory, Suzanne
; APPLICANT: Adams, Jerry
; APPLICANT: Print, Cris
; APPLICANT: Gibson, Leonie
; APPLICANT: Koentgen, Frank
; TITLE OF INVENTION: A METHOD OF TREATMENT AND AN ANIMAL MODEL USEFUL FOR
; FILE REFERENCE: 13464
; CURRENT APPLICATION NUMBER: US/11/301,951
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US/09/508,745
```



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2006, 12:24:51 ; Search time 181 Seconds  
(without alignments)  
424.827 Million cell updates/sec

Title: US-09-716-395-2

Perfect score: 897

Sequence: 1 MAHAGRTGYDNRREIVMKYIH.....WTQDNGGWDFAFVELYGPSMR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	796	88.7	200	5	US-10-981-873-45
2	781.5	87.1	239	2	US-08-726-211-5
3	781.5	87.1	239	3	US-09-993-420A-8
4	781.5	87.1	239	4	US-10-141-618-12
5	781.5	87.1	239	4	US-10-053-645A-21
6	781.5	87.1	239	4	US-10-387-961A-5
7	781.5	87.1	239	4	US-10-003-632C-1
8	781.5	87.1	239	4	US-10-003-632C-3
9	781.5	87.1	239	4	US-10-148-953A-1
10	781.5	87.1	239	5	US-10-825-282-46
11	781.5	87.1	239	5	US-10-961-458-21
12	778.5	86.8	239	4	US-10-148-953A-2
13	778.5	86.8	239	4	US-10-148-953A-4
14	778.5	86.8	239	4	US-10-297-321-2
15	777.5	86.7	239	4	US-10-148-953A-5
16	775.5	86.5	239	4	US-10-148-953A-3
17	769.5	85.8	239	4	US-10-277-693A-10
18	769.5	85.8	239	4	US-10-003-632C-10
19	769.5	85.8	239	4	US-10-003-632C-13
20	769.5	85.8	239	6	US-11-037-713-5
21	763.5	85.1	239	4	US-10-101-482-12
22	763.5	85.1	239	4	US-10-072-830-2
23	763.5	85.1	239	4	US-10-450-366-4
24	763.5	85.1	239	4	US-10-770-668-16
25	763.5	85.1	239	5	US-10-887-066-2
26	763.5	85.1	239	6	US-11-082-485-12
27	757	84.4	236	4	US-10-087-192-1953

28	753.5	84.0	239	4	US-10-659-705-4	Sequence 4, Appli
29	752	83.8	236	4	US-10-277-693A-11	Sequence 11, Appl
30	718.5	80.1	205	4	US-08-726-211-7	Sequence 7, Appli
31	718.5	80.1	205	3	US-09-952-278-4	Sequence 4, Appli
32	718.5	80.1	205	4	US-10-053-645A-23	Sequence 23, Appli
33	718.5	80.1	205	4	US-10-387-961A-7	Sequence 7, Appli
34	718.5	80.1	205	4	US-10-003-632C-2	Sequence 2, Appli
35	718.5	80.1	205	4	US-10-003-632C-11	Sequence 11, Appli
36	718.5	80.1	205	5	US-10-961-458-23	Sequence 23, Appli
37	706.5	78.8	205	4	US-10-087-192-1956	Sequence 1956, Ap
38	704.5	78.5	155	4	US-10-158-769-1	Sequence 1, Appli
39	704.5	78.5	155	4	US-10-729-156-1	Sequence 1, Appli
40	701.5	78.2	233	4	US-10-659-705-3	Sequence 3, Appli
41	608	67.8	154	4	US-10-007-573-3	Sequence 3, Appli
42	584	65.1	231	5	US-10-450-763-40224	Sequence 40224, A
43	556	62.0	152	4	US-10-158-769-2	Sequence 2, Appli
44	556	62.0	152	4	US-10-729-156-2	Sequence 2, Appli
45	546	60.9	199	4	US-10-402-017-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-981-873-45  
; Sequence 45, Application US/10981873  
; Publication No. US20050250680A1  
; GENERAL INFORMATION:  
; APPLICANT: Walensky, Loren D.  
; APPLICANT: Korameyer, Stanley J.  
; APPLICANT: Verdine, Gregory  
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND  
; FILE REFERENCE: 00530-124001  
; CURRENT APPLICATION NUMBER: US/10/981,873  
; PRIOR FILING DATE: 2004-11-05  
; PRIOR APPLICATION NUMBER: US 60/517,848  
; PRIOR FILING DATE: 2003-11-05  
; PRIOR APPLICATION NUMBER: US 60/591,548  
; PRIOR FILING DATE: 2004-07-27  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 200  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-981-873-45

Query Match	88.7%	Score 796;	DB 5;	Length 200;
Best Local Similarity	90.5%	Pred. No. 1.3e-80;		
Matches 152;	Conservative	0;	Mismatches 14;	Indels 2;
Gaps 1;				
QY	1	MAHAGRTGYDNRREIVMKYIHKLSQSGYEWADGDDVEENRTEAPEGTE--SEVVHIALRQ	58	
Db	1	MAHAGRTGYDNRREIVMKYIHKLSQSGYEWADGDDVEENRTEAPEGTE--SEVVHIALRQ	60	
QY	59	AGDDFSRRYRGDFAEWSSQLHLPETARGRFATVVEELPRDGVNMGRIIVAFEFEGVMCV	118	
Db	61	AGDDFSRRYRGDFAEWSSQLHLPETARGRFATVVEELPRDGVNMGRIIVAFEFEGVMCV	120	
QY	119	ESVNSREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDFAFVELYGPSMR	166	
Db	121	ESVNSREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDFAFVELYGPSMR	168	

RESULT 2

US-08-726-211-5  
; Sequence 5, Application US/08726211  
; Publication No. US20030012812A1  
; GENERAL INFORMATION:  
; APPLICANT: Tormo, Mar  
; APPLICANT: Tari, Ana M.  
; APPLICANT: Lopez-Berestein, Gabriel



Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 180

QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166

Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 5

US-10-053-645A-21

; Sequence 21, Application US/10053645A

; Publication No. US20030176376A1

; GENERAL INFORMATION:

; APPLICANT: Robert E. Klem

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A

; TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2

; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF

; FILE REFERENCE: 10412-022-999

; CURRENT APPLICATION NUMBER: US/10/053,645A

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: 60/263,244

; PRIOR FILING DATE: 2001-01-22

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 21

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-053-645A-21

Query Match 87.1%; Score 781.5; DB 4; Length 239;

Best Local Similarity 73.4%; Pred. No. 7.2e-79;

Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45

Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAPAGIFSSQPGHTPHPA 60

QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79

Db 61 ASRDPVARTSPLQTPAAPGAAGPALSPVPPVVHLALROAGDDFSRRYRGDFAEMSSQLH 120

QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 139

Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 180

QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166

Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 6

US-10-387-961A-5

; Sequence 5, Application US/10387961A

; Publication No. US20030219474A1

; GENERAL INFORMATION:

; APPLICANT: TORMO, MAR

; APPLICANT: TARI, ANA M.

; APPLICANT: LOPEZ-BERESTIN, GABRIEL

; TITLE OF INVENTION: INHIBITION OF BCL-2 PROTEIN EXPRESSION BY LIPOSOMAL

; TITLE OF INVENTION: ANTISENSE OLIGODEOXYNUCLEOTIDES

; FILE REFERENCE: UTXC:504USD1

; CURRENT APPLICATION NUMBER: US/10/387,961A

; CURRENT FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: 08/726,211

; PRIOR FILING DATE: 1996-10-04

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-10-387-961A-5

Query Match 87.1%; Score 781.5; DB 4; Length 239;

Best Local Similarity 73.4%; Pred. No. 7.2e-79;

Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45

Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAPAGIFSSQPGHTPHPA 60

QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79

Db 61 ASRDPVARTSPLQTPAAPGAAGPALSPVPPVVHLALROAGDDFSRRYRGDFAEMSSQLH 120

QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 139

Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 180

QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166

Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 7

US-10-003-632C-1

; Sequence 1, Application US/10003632C

; Publication No. US20040043028A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Chichang; Ly, Celia; Moore, Gordon; Chi, Ximei

; TITLE OF INVENTION: Methods and Compositions for Enhanced Protein Expression and/or

; TITLE OF INVENTION: Cultured Cells Using Co-Transcription of a Bcl2 Encoding Nuclei

; FILE REFERENCE: CEN0269

; CURRENT APPLICATION NUMBER: US/10/003,632C

; CURRENT FILING DATE: 2001-11-02

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver 3.1

; SEQ ID NO 1

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-003-632C-1

Query Match 87.1%; Score 781.5; DB 4; Length 239;

Best Local Similarity 73.4%; Pred. No. 7.2e-79;

Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45

Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAPAGIFSSQPGHTPHPA 60

QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79

Db 61 ASRDPVARTSPLQTPAAPGAAGPALSPVPPVVHLALROAGDDFSRRYRGDFAEMSSQLH 120

QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 139

Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 180

QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166

Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 8

US-10-003-632C-3

; Sequence 3, Application US/10003632C

; Publication No. US20040043028A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Chichang; Ly, Celia; Moore, Gordon; Chi, Ximei

; TITLE OF INVENTION: Methods and Compositions for Enhanced Protein Expression and/or

; TITLE OF INVENTION: Cultured Cells Using Co-Transcription of a Bcl2 Encoding Nuclei

; FILE REFERENCE: CEN0269



```
; CURRENT APPLICATION NUMBER: US/10/003,632C
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 3
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-632C-3

Query Match      87.1%; Score 781.5; DB 4; Length 239;
Best Local Similarity 73.4%; Pred. No. 7.2e-79;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNREIVMKYIHYKLSQRYEWDAAGD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYDNREIVMKYIHYKLSQRYEWDAAGDVGAAAPGAPGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPVPVPHLALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
DB 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 9
US-10-148-953A-1
; Sequence 1, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7398/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JPO07/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-953A-1

Query Match      87.1%; Score 781.5; DB 4; Length 239;
Best Local Similarity 73.4%; Pred. No. 7.2e-79;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNREIVMKYIHYKLSQRYEWDAAGD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYDNREIVMKYIHYKLSQRYEWDAAGDVGAAAPGAPGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPVPVPHLALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
DB 181 LNRHLHTWIQDNGWDADFVELYGPMSR 166
```

```
DB 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 10
US-10-825-282-46
; Sequence 46, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-825-282-46

Query Match      87.1%; Score 781.5; DB 5; Length 239;
Best Local Similarity 73.4%; Pred. No. 7.2e-79;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNREIVMKYIHYKLSQRYEWDAAGD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYDNREIVMKYIHYKLSQRYEWDAAGDVGAAAPGAPGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPVPVPHLALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
DB 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 11
US-10-961-458-21
; Sequence 21, Application US/10961458
; Publication No. US20050170377A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
; FILE REFERENCE: 04040/1200990-US7
; CURRENT APPLICATION NUMBER: US/10/961,458
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US/10/961,458
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US 09/375,514
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 09/080,285
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: US 08/465,485
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/124,256
; PRIOR FILING DATE: 1993-09-20
```



```
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant Bcl-2
; OTHER INFORMATION: Gene, D34A
US-10-297-321-2
```

```
Query Match      86.8%; Score 778.5; DB 4; Length 239;
Best Local Similarity 74.4%; Pred. No. 1.6e-78;
Matches 154; Conservative 2; Mismatches 10; Indels 41; Gaps 3;

Qy      1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAG-----DVEENRTBAPE 33
Db      1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGVGAAPGAAAPAGGIFSSQPGHTHPA 60

Qy      34 ---DDVEEN---RTEAPEGTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db      61 ASRDPVARTSLQTPAAPGAAAGPALSPPVPVHLLRQAGDDFSRRYRGDFAEMSSQLH 120

Qy      80 LTPFTARGRFATVVEELFRDGVNMGRIVAFEFEGGVMCVSVNREMSPLVDNIALWMTEY 139
Db      121 LTPFTARGRFATVVEELFRDGVNMGRIVAFEFEGGVMCVSVNREMSPLVDNIALWMTEY 180

Qy      140 LNRHLHTWIQDNGGWDADFVELYGPMSR 166
Db      181 LNRHLHTWIQDNGGWDADFVELYGPMSR 207
```

```
RESULT 15
US-10-148-953A-5
; Sequence 5, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: modified Bcl-2 protein
US-10-148-953A-5
```

```
Query Match      86.7%; Score 777.5; DB 4; Length 239;
Best Local Similarity 72.9%; Pred. No. 2e-78;
Matches 151; Conservative 2; Mismatches 13; Indels 41; Gaps 2;

Qy      1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGD-----DVEENRTBAPE 45
Db      1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGVGAAPGAAAPAGGIFSSQPGHTHPA 60

Qy      46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db      61 ASRDPVARTSLQTPAAPGAAAGPALSPPVPVHLLRQAGDDFSRRYRGDFAEMSSQLH 120

Qy      80 LTPFTARGRFATVVEELFRDGVNMGRIVAFEFEGGVMCVSVNREMSPLVDNIALWMTEY 139
```

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2006, 12:12:56 ; Search time 50 Seconds  
(without alignments)  
290.602 Million cell updates/sec

Title: US-09-716-395-2

Perfect score: 897

Sequence: 1 MAHAGRTGYDNRREIVMKYIH.....WIQDNGWDFAVELYGPMSR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/iaa/5 COMB.pcp:\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pcp:\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pcp:\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/iaa/H COMB.pcp:\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pcp:\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pcp:\*
- 7: /EMC Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	781.5	87.1	239	1 US-08-333-565-51	Sequence 51, Appl
2	781.5	87.1	239	1 US-08-248-819A-10	Sequence 12, Appl
3	781.5	87.1	239	1 US-08-690-095-4	Sequence 4, Appl
4	781.5	87.1	239	1 US-08-465-485A-21	Sequence 21, Appl
5	781.5	87.1	239	1 US-08-861-479-51	Sequence 51, Appl
6	781.5	87.1	239	1 US-08-365-486A-15	Sequence 15, Appl
7	781.5	87.1	239	1 US-08-337-646A-12	Sequence 12, Appl
8	781.5	87.1	239	2 US-09-113-789-4	Sequence 4, Appl
9	781.5	87.1	239	2 US-09-080-285-21	Sequence 21, Appl
10	781.5	87.1	239	2 US-08-927-326-12	Sequence 12, Appl
11	781.5	87.1	239	2 US-08-880-342-15	Sequence 15, Appl
12	781.5	87.1	239	2 US-09-234-186-8	Sequence 8, Appl
13	781.5	87.1	239	2 US-09-724-426-20	Sequence 20, Appl
14	781.5	87.1	239	2 US-09-724-426-21	Sequence 21, Appl
15	781.5	87.1	239	2 US-09-233-527-8	Sequence 8, Appl
16	781.5	87.1	239	2 US-09-724-425-21	Sequence 21, Appl
17	781.5	87.1	239	2 US-09-993-420A-8	Sequence 8, Appl
18	781.5	87.1	239	2 US-10-003-632C-1	Sequence 1, Appl
19	781.5	87.1	239	2 US-10-003-632C-3	Sequence 3, Appl
20	781.5	87.1	239	2 US-08-726-211-5	Sequence 5, Appl
21	781.5	87.1	239	3 US-09-375-514B-21	Sequence 21, Appl
22	781.5	87.1	239	5 PCT-US93-05651-5	Sequence 5, Appl
23	781.5	87.1	239	7 5459251-2	Patent No. 5459251
24	781.5	87.1	239	7 5506344-2	Patent No. 5506344
25	771.5	86.0	239	1 US-08-405-702A-12	Sequence 12, Appl
26	769.5	85.8	239	1 US-08-112-208C-10	Sequence 10, Appl

27	769.5	85.8	239	1 US-08-248-819A-10	Sequence 10, Appl
28	769.5	85.8	239	1 US-08-337-646A-10	Sequence 10, Appl
29	769.5	85.8	239	1 US-08-856-531-10	Sequence 10, Appl
30	769.5	85.8	239	1 US-08-856-034-10	Sequence 10, Appl
31	769.5	85.8	239	2 US-09-127-048-8	Sequence 8, Appl
32	769.5	85.8	239	2 US-08-927-326-10	Sequence 10, Appl
33	769.5	85.8	239	2 US-09-379-820A-10	Sequence 10, Appl
34	769.5	85.8	239	2 US-10-003-632C-10	Sequence 10, Appl
35	769.5	85.8	239	2 US-10-003-632C-13	Sequence 13, Appl
36	763.5	85.1	239	1 US-08-607-269-20	Sequence 20, Appl
37	763.5	85.1	239	1 US-08-471-058-12	Sequence 12, Appl
38	763.5	85.1	239	2 US-08-471-057-12	Sequence 12, Appl
39	763.5	85.1	239	2 US-08-470-865-12	Sequence 12, Appl
40	763.5	85.1	239	2 US-09-155-327G-11	Sequence 11, Appl
41	763.5	85.1	239	2 US-09-633-200-12	Sequence 12, Appl
42	763.5	85.1	239	5 PCT-US95-04600-20	Sequence 20, Appl
43	763	85.1	232	1 US-08-408-095-17	Sequence 17, Appl
44	761	84.8	232	1 US-08-408-095-18	Sequence 18, Appl
45	759	84.6	236	1 US-08-607-269-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1  
US-08-333-565-51  
; Sequence 51, Application US/083333565  
; Patent No. 5622852  
; GENERAL INFORMATION:  
; APPLICANT: KORMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333,565  
; FILING DATE: 31-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-333-565-51

Query Match 87.1%; Score 781.5; DB 1; Length 239;  
Best Local Similarity 73.4%; Pred. No. 1e-85;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRGEWDAGD-----DVEENRTEAPE 45  
|||||  
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRGEWDAGDVGAAAPGAPGIFSSQPGHTPHPA 60  
|||||

```
Qy 46 CTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASRDPVARTSPLOTTPAAPAAAGPALSPPVPVHLLALRQAGDDFSRRYRGDFAEMSSQLH 120
Qy 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 180
Qy 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
Db 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 2
US-08-248-819A-12
; Sequence 12, Application US/08248819A
; Patent No. 5700638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,819A
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-248-819A-12

Query Match 87.1%; Score 781.5; DB 1; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

Qy 1 MAHAGRTGYDNREIVMKYIHYKLSQRGYEWADG-----DVEENRTEAPE 45
Db 1 MAHAGRTGYDNREIVMKYIHYKLSQRGYEWADGVAAPGAAPAGIFFSQPGHTHPA 60
Qy 46 CTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASRDPVARTSPLOTTPAAPAAAGPALSPPVPVHLLALRQAGDDFSRRYRGDFAEMSSQLH 120
Qy 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 180
Qy 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
Db 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 4
US-08-465-485A-21
; Sequence 21, Application US/08465485A
; Patent No. 5831066
```

```
Db 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 3
US-08-690-095-4
; Sequence 4, Application US/08690095
; Patent No. 5792648
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,095
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 179367
; US-08-690-095-4

Query Match 87.1%; Score 781.5; DB 1; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

Qy 1 MAHAGRTGYDNREIVMKYIHYKLSQRGYEWADG-----DVEENRTEAPE 45
Db 1 MAHAGRTGYDNREIVMKYIHYKLSQRGYEWADGVAAPGAAPAGIFFSQPGHTHPA 60
Qy 46 CTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASRDPVARTSPLOTTPAAPAAAGPALSPPVPVHLLALRQAGDDFSRRYRGDFAEMSSQLH 120
Qy 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 180
Qy 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
Db 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 4
US-08-465-485A-21
; Sequence 21, Application US/08465485A
; Patent No. 5831066
```

GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION NUMBER: US 08/465,485A  
FILING DATE: 20-SEP-1993  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear,  
MOLECULE TYPE: protein  
US-08-465-485A-21

Query Match 87.1%; Score 781.5; DB 1; Length 239;  
Best Local Similarity 73.4%; Pred. No. 1e-85;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;  
QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAPAGPFISSQPGHTPHFA 60  
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPPVHLLALROAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LTPFTARGFATVVEELFRDGVNMGRIVAFFFGVCMCVESVNREMSPLVDNLALWMTEY 139  
DB 121 LTPFTARGFATVVEELFRDGVNMGRIVAFFFGVCMCVESVNREMSPLVDNLALWMTEY 180  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
DB 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 5  
US-08-661-479-51  
Sequence 51, Application US/08661479  
Patent No. 5834209  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH

TITLE OF INVENTION: REGULATOR  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 11-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: US 08/333,565  
FILING DATE: 31-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000700  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-661-479-51

Query Match 87.1%; Score 781.5; DB 1; Length 239;  
Best Local Similarity 73.4%; Pred. No. 1e-85;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;  
QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAPAGPFISSQPGHTPHFA 60  
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPPVHLLALROAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LTPFTARGFATVVEELFRDGVNMGRIVAFFFGVCMCVESVNREMSPLVDNLALWMTEY 139  
DB 121 LTPFTARGFATVVEELFRDGVNMGRIVAFFFGVCMCVESVNREMSPLVDNLALWMTEY 180  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
DB 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 6  
US-08-365-486A-15  
Sequence 15, Application US/08365486A  
Patent No. 5834306  
GENERAL INFORMATION:  
APPLICANT: Webster, Keith A.  
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
TITLE OF INVENTION: Therapeutic Constructs  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA

```

; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-365-486A-15

Query Match 87.1%; Score 781.5; DB 1; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYDNREIVMKYIHYKLSQRYEWDAGDVGAAAPGGAAPAGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTPLQTPAAPGAAAGPALSPVPPVHVALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFGVGMCVESVNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFGVGMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGWDADFVELYGPSMR 166
DB 181 LNRHLHTWIQDNGWDADFVELYGPSMR 207

RESULT 7
US-08-337-646A-12
; Sequence 12, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,646A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,819

; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-365-486A-15

Query Match 87.1%; Score 781.5; DB 1; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYDNREIVMKYIHYKLSQRYEWDAGDVGAAAPGGAAPAGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTPLQTPAAPGAAAGPALSPVPPVHVALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFGVGMCVESVNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFGVGMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGWDADFVELYGPSMR 166
DB 181 LNRHLHTWIQDNGWDADFVELYGPSMR 207

RESULT 8
US-09-113-789-4
; Sequence 4, Application US/09113789
; Patent No. 6034219
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,789
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/690,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
```



## TELECOMMUNICATION INFORMATION:

NAME: Fortney, Andrew D.  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 179367  
US-09-113-789-4

Query Match 87.1%; Score 781.5; DB 2; Length 239;  
Best Local Similarity 73.4%; Pred. No. 1e-85;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;  
QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAPGIFSSQPGHTPHEA 60  
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPVPPVVHLLALROAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LPTFTARGFATVVEELFRDGVNMGRIVAFFBFGGVMCVESVNREMSPLVDNIALMWTY 139  
DB 121 LPTFTARGFATVVEELFRDGVNMGRIVAFFBFGGVMCVESVNREMSPLVDNIALMWTY 180  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
DB 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

## RESULT 9

US-09-080-285-21  
Sequence 21, Application US/09080285  
Patent No. 6040181  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/080,285  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,485  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-080-285-21

Query Match 87.1%; Score 781.5; DB 2; Length 239;  
Best Local Similarity 73.4%; Pred. No. 1e-85;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;  
QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAPGIFSSQPGHTPHEA 60  
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPVPPVVHLLALROAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LPTFTARGFATVVEELFRDGVNMGRIVAFFBFGGVMCVESVNREMSPLVDNIALMWTY 139  
DB 121 LPTFTARGFATVVEELFRDGVNMGRIVAFFBFGGVMCVESVNREMSPLVDNIALMWTY 180  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
DB 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

## RESULT 10

US-08-927-326-12  
Sequence 12, Application US/08927326  
Patent No. 6184202  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: CELL DEATH REGULATORS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/927,326  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,646  
FILING DATE: 10-NOV-1994  
APPLICATION NUMBER: US 08/248,819  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/112,208  
FILING DATE: 26-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000620  
TELECOMMUNICATION INFORMATION:

```
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-927-326-12

Query Match      87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAAPAGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASROPVARTSPLQTPAAPGAAAGPALSPPVPPVHLALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 180
QY 140 LNRHLTWIQDNGWDADFVELYGFMSR 166
Db 181 LNRHLTWIQDNGWDADFVELYGFMSR 207

RESULT 11
US-08-880-342-15
Sequence 15, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-880-342-15

Query Match      87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAAPAGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASROPVARTSPLQTPAAPGAAAGPALSPPVPPVHLALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 180
QY 140 LNRHLTWIQDNGWDADFVELYGFMSR 166
Db 181 LNRHLTWIQDNGWDADFVELYGFMSR 207

RESULT 12
US-09-234-186-8
Sequence 8, Application US/09234186
Patent No. 6312947
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Hengartner, Michael
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 01997/201005
CURRENT APPLICATION NUMBER: US/09/234,186
CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: 07/898,933
EARLIER FILING DATE: 1992-06-12
EARLIER APPLICATION NUMBER: 07/927,681
EARLIER FILING DATE: 1992-08-10
EARLIER APPLICATION NUMBER: 08/288,295
EARLIER FILING DATE: 1994-08-10
EARLIER APPLICATION NUMBER: 08/801,248
EARLIER FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-234-186-8

Query Match      87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAAPAGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASROPVARTSPLQTPAAPGAAAGPALSPPVPPVHLALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 180
QY 140 LNRHLTWIQDNGWDADFVELYGFMSR 166
Db 181 LNRHLTWIQDNGWDADFVELYGFMSR 207
```

Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 180  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

## RESULT 13

US-09-724-426-20  
; Sequence 21, Application US/09724426  
; Patent No. 6414134  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John  
; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression  
; FILE REFERENCE: 10412-024  
; CURRENT APPLICATION NUMBER: US/09/724,426  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 20  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-426-20

Query Match 87.1%; Score 781.5; DB 2; Length 239;  
Best Local Similarity 73.4%; Pred. No. 1e-85;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDGAAPGAPGIFSSQFGHTPHPA 60  
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
Db 61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPPVHLLALROAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 139  
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 180  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

## RESULT 14

US-09-724-426-21  
; Sequence 21, Application US/09724426  
; Patent No. 6414134  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John  
; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression  
; FILE REFERENCE: 10412-024  
; CURRENT APPLICATION NUMBER: US/09/724,426  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 21  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-426-21

Query Match 87.1%; Score 781.5; DB 2; Length 239;  
Best Local Similarity 73.4%; Pred. No. 1e-85;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDGAAPGAPGIFSSQFGHTPHPA 60  
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79

Db 61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPPVHLLALROAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 139  
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 180  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

## RESULT 15

US-09-233-527-8  
; Sequence 8, Application US/09233527  
; Patent No. 6465617  
; GENERAL INFORMATION:  
; APPLICANT: Horvitz, H. Robert  
; APPLICANT: Hengartner, Michael  
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A  
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND  
; TITLE OF INVENTION: USES THEREFOR  
; FILE REFERENCE: 01997/201004  
; CURRENT APPLICATION NUMBER: US/09/233,527  
; CURRENT FILING DATE: 1999-01-20  
; PRIOR APPLICATION NUMBER: 07/898,933  
; PRIOR FILING DATE: 1992-06-12  
; PRIOR APPLICATION NUMBER: 07/927,681  
; PRIOR FILING DATE: 1992-08-10  
; PRIOR APPLICATION NUMBER: 08/288,295  
; PRIOR FILING DATE: 1994-08-10  
; PRIOR APPLICATION NUMBER: 08/801,248  
; PRIOR FILING DATE: 1997-02-19  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-233-527-8

Query Match 87.1%; Score 781.5; DB 2; Length 239;  
Best Local Similarity 73.4%; Pred. No. 1e-85;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDGAAPGAPGIFSSQFGHTPHPA 60  
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
Db 61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPPVHLLALROAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 139  
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 180  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

Search completed: December 30, 2006, 12:14:19  
JOB time : 51 secs

**This Page Blank (uspto)**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2006, 12:03:31 ; Search time 199 Seconds  
(without alignments)  
381.397 Million cell updates/sec

Title: US-09-716-395-2

Perfect score: 897

Sequence: 1 MAHAGRTGYDNRREIVMKYIH.....WIQDNGWDFAVELYGFPSMR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_8:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*  
10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	897	100.0	166	5	ABG78476 Human Bcl
2	781.5	87.1	239	1	ABP80987 Sequence
3	781.5	87.1	239	2	AAR42312 Bcl-2 onc
4	781.5	87.1	239	2	AAR70331 Human bcl
5	781.5	87.1	239	2	AAR71404 Human bcl
6	781.5	87.1	239	2	AAR40217 Human bcl
7	781.5	87.1	239	2	AAW87812 A human B
8	781.5	87.1	239	4	AAG64035 Human Bcl
9	781.5	87.1	239	4	ABY74129 Human bcl
10	781.5	87.1	239	5	AAE08573 Human Bcl
11	781.5	87.1	239	5	ABG31127 Bcl-2 ant
12	781.5	87.1	239	5	ABG78477 Human Bcl
13	781.5	87.1	239	5	ABY78197 Amino aci
14	781.5	87.1	239	5	ABY78196 Amino aci
15	781.5	87.1	239	5	ABY75986 Protein s
16	781.5	87.1	239	6	AAE37650 Bcl2 rela
17	781.5	87.1	239	6	AAE37652 Bcl2 rela
18	781.5	87.1	239	6	ABY82742 Human Bcl
19	781.5	87.1	239	7	ABU63582 Human Bcl
20	781.5	87.1	239	8	ADG87141 Human Bcl
21	781.5	87.1	239	8	ADL69723 Human Bcl
22	781.5	87.1	239	8	ADL69721 Human Bcl
23	781.5	87.1	239	8	ADU22905 Human apo

24	781.5	87.1	239	9	ADW13850 Human bcl
25	781.5	87.1	272	2	AAZ21120 Human bcl
26	778.5	86.8	239	2	AAR47344 Human onc
27	778.5	86.8	239	4	AAG64036 Human Bcl
28	778.5	86.8	239	4	AAG64038 Human Bcl
29	778.5	86.8	239	5	ABY05227 Human D34
30	778.5	86.8	239	7	ADF28076 Mutant Bc
31	777.5	86.7	239	4	AAG64039 Human Bcl
32	775.5	86.5	239	4	AAG64037 Human Bcl
33	771.5	86.0	239	2	AAW02383 Human Bcl
34	769.5	85.8	239	2	AAW87810 A human B
35	769.5	85.8	239	4	AAE35130 Human Bcl
36	769.5	85.8	239	4	AAE374127 Human Bcl
37	769.5	85.8	239	5	ABG78479 Human Bcl
38	769.5	85.8	239	5	ABG78478 Human Bcl
39	769.5	85.8	239	5	AAU76553 Human Bcl
40	769.5	85.8	239	6	AAE37661 Human Bcl
41	769.5	85.8	239	6	AAE37658 Bcl2 rela
42	769.5	85.8	239	7	ADD45440 Human Pro
43	769.5	85.8	239	7	ADF60831 Human Bcl
44	769.5	85.8	239	7	ADI63113 Human apo
45	769.5	85.8	239	8	ADJ66631 Bcl-2 pro

#### ALIGNMENTS

##### RESULT 1

ABG78476  
ID ABG78476 standard; protein; 166 AA.  
XX  
AC ABG78476;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Human Bcl2 mutant protein.  
XX  
KW Human; Bcl2; BclX1; programmed cell death; apoptosis; mutant; mteuin.  
XX  
OS Homo sapiens.  
XX  
SS Synthetic.  
XX  
PN WO200240530-A2..  
XX  
PD 23-MAY-2002.  
XX  
PF 15-NOV-2001; 2001WO-US045693.  
XX  
PR 20-NOV-2000; 2000US-00716395.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Fesik SW, Petros AM, Yoon H, Nettesheim DG;  
XX  
DR WPI; 2002-490141/52.  
XX  
PT New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,  
XX  
PT useful in biological assays to identify substances that block the ability  
XX  
PS of Bcl-2 to inhibit programmed cell death or apoptosis.  
XX  
XX Claim 8; Page 20; 36pp; English.  
XX  
CC This invention relates to a novel mutant protein which is derived from a  
XX  
CC wild type human Bcl-2 protein. The mutant is created by replacing a  
XX  
CC sequence of amino acid residues comprising a flexible loop from the wild  
XX  
CC type Bcl-2 protein with an amino acid sequence comprising at least two  
XX  
CC acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue  
XX  
CC shown in the specification. The invention also comprises an assay for  
XX  
CC identifying substances that bind to the Bcl-2 protein. The protein  
XX  
CC sequences of the invention are useful in biological assays to identify  
XX  
CC substances that block the ability of Bcl-2 to inhibit programmed cell  
XX  
CC death or apoptosis. The present sequence represents a human Bcl2 mutant  
XX  
CC protein used in the invention





```
XX SQ Sequence 239 AA;
Query Match 87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 4e-82;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYNREIVMKYIHYKLSQRCYEWDAKD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYNREIVMKYIHYKLSQRCYEWDAKDVGAAAPGAPGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTSPLQTPAAGAAAGPALSPVPVPHALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGGWDFAVELYGPMSR 166
DB 181 LNRHLHTWIQDNGGWDFAVELYGPMSR 207

RESULT 6
AAW40217
ID AAW40217 standard; peptide; 239 AA.
XX AAW40217;
AC
XX
DT 07-JUL-1998 (first entry)
DE Human bcl-2.
XX
KW TMAH; apoptosis; osteoarthritis; c-type lectin; A1 family; diagnosis;
KW treatment.
XX
OS Homo sapiens.
XX
PN WO9804585-A2.
XX
PD 05-FEB-1998.
XX
PF 22-JUL-1997; 97WO-US013077.
XX
PR 31-JUL-1996; 96US-00690095.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Au-Young J, Goli SK;
XX
DR WPI; 1998-130617/12.
XX
PT Human macrophage antigen - used for decreasing apoptosis associated with
PT osteoarthritis.
XX
PS Disclosure; Page 43; 58pp; English.
XX
CC The human bcl-2 peptide is one of a group of peptides with which the
CC human macrophage antigen (TMAH) (AAW40215) has 20% homology. The homology
CC which TMAH shares with the other A1 family members includes conserved
CC residues at F27, P35, R119, W139, F146 AND W214. The structural homology
CC between the mammalian A1 and C-type lectins and TMAH provides information
CC on the structural and physical properties of both the TMAH gene and
CC protein. This is used in the development of TMAH as a diagnostic tool and
CC as a method of treating diseases associated with expression of TMAH
XX
SQ Sequence 239 AA;
Query Match 87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 4e-82;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYNREIVMKYIHYKLSQRCYEWDAKD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYNREIVMKYIHYKLSQRCYEWDAKDVGAAAPGAPGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTSPLQTPAAGAAAGPALSPVPVPHALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGGWDFAVELYGPMSR 166
DB 181 LNRHLHTWIQDNGGWDFAVELYGPMSR 207

RESULT 7
AAW87812
ID AAW87812 standard; protein; 239 AA.
XX
AC AAW87812;
XX
DT 10-MAR-1999 (first entry)
DE A human Bcl-2-alpha protein.
XX
KW Human; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
KW bcl-2-related function; apoptosis; dimer; Bcl-xL; Mcl-1; A1.
XX
OS Homo sapiens.
XX
PN US5856171-A.
XX
PD 05-JAN-1999.
XX
PF 10-NOV-1994; 94US-00337646.
XX
PR 26-AUG-1993; 93US-00112208.
XX
PR 25-MAY-1994; 94US-00248819.
XX
PA (UNIW ) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR WPI; 1999-105119/09.
XX
PT DNA composition encoding bcl-2 two-hybrid and reporter system - for
XX identifying modulators of bcl-2 function.
XX
PS Disclosure; Col 29; 105pp; English.
XX
CC The present sequence represents a human Bcl-2-alpha protein. The
CC specification also describes Bcl-2 associated proteins designated Bax.
CC The Bax protein is used in a composition which comprises a bcl-2 family
CC member polypeptide, a naturally occurring Bax polypeptide and an antibody
CC that binds to the Bax polypeptide. The specification also describes a
CC composition comprising a hybrid protein comprising an activator domain of
CC a transcriptional activator protein and a bcl-2 family member having a
CC BHL domain and a BH2 domain; another hybrid protein comprising a DNA-
CC binding domain of the transcriptional activator protein and a second bcl-
CC 2 family member having a BHL domain and a BH2 domain; and a reporter gene
CC linked to a transcriptional regulatory element whose transcriptional
CC activity is dependent on the presence or absence of a dimer of the two
CC hybrid proteins. The bcl-2 family members are selected from naturally
CC occurring Bcl-2, Bcl-xL, Bax, Mcl-1, A1, fragments thereof, and mutants
CC having a mutation in the BHL and/or BH2 domain that alters intermolecular
CC binding of the two bcl-2 family members. The compositions are used to
CC identify modulators of bcl-2-related function, e.g. substances that
CC inhibit binding of Bax to bcl-2, which would be potentially useful as
CC drugs for modulating apoptosis
XX
SQ Sequence 239 AA;
```



Query Match 87.1%; Score 781.5; DB 2; Length 239;  
Best Local Similarity 73.4%; Pred. No. 4e-82;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRIVMKYIHYKLSQSGYEWDAAGD-----DVEENRTEAPE 45  
DB 1 MAHAGRTGYDNRIVMKYIHYKLSQSGYEWDAAGDVGAAAPGAPGIFSSQPGHTPHPA 60  
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPPVHLLALRQAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LTPFTARGFPATVVEELFRDGVNMGRIVAFFFGGVMCVESVNREMSPLVDNIALWMTEY 139  
DB 121 LTPFTARGFPATVVEELFRDGVNMGRIVAFFFGGVMCVESVNREMSPLVDNIALWMTEY 180  
QY 140 LNRHLHTWIQDNGWDFAVELYGPSMR 166  
DB 181 LNRHLHTWIQDNGWDFAVELYGPSMR 207

## RESULT 8

AAG64035

ID AAG64035 standard; protein; 239 AA.

AC AAG64035;

XX 10-SEP-2001 (first entry)

DT 10-SEP-2001 (first entry)

DE Human Bcl-2 protein.

XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant.

XX Homo sapiens.

XX WO200142459-A1.

XX 14-JUN-2001.

XX 07-DEC-2000; 2000WO-JP008667.

XX 09-DEC-1999; 99JP-00350427.

XX (HISM ) HISAMITSU PHARM CO LTD.

XX Shibazaki F, Kuma H;

XX WPI; 2001-381681/40.

XX N-PSDB; AAH45293.

XX New apoptosis inhibitors, useful for treating apoptosis related disorders.

XX Claim 1; Page 29-30; 43pp; Japanese.

XX The invention relates to an apoptosis inhibitor comprising the amino acid sequence of Bcl-2 protein in which at least one serine residue is substituted by alanine or aspartic acid. The protein has increased apoptosis inhibitory activity compared with the wild type Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment of disorders caused by apoptosis. The present sequence is the wild type human Bcl-2 protein

SQ Sequence 239 AA;

Query Match 87.1%; Score 781.5; DB 4; Length 239;  
Best Local Similarity 73.4%; Pred. No. 4e-82;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRIVMKYIHYKLSQSGYEWDAAGD-----DVEENRTEAPE 45  
DB 1 MAHAGRTGYDNRIVMKYIHYKLSQSGYEWDAAGDVGAAAPGAPGIFSSQPGHTPHPA 60

QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPPVHLLALRQAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LTPFTARGFPATVVEELFRDGVNMGRIVAFFFGGVMCVESVNREMSPLVDNIALWMTEY 139  
DB 121 LTPFTARGFPATVVEELFRDGVNMGRIVAFFFGGVMCVESVNREMSPLVDNIALWMTEY 180  
QY 140 LNRHLHTWIQDNGWDFAVELYGPSMR 166  
DB 181 LNRHLHTWIQDNGWDFAVELYGPSMR 207

## RESULT 9

AAB74129

ID AAB74129 standard; protein; 239 AA.

AC AAB74129;

XX 22-MAY-2001 (first entry)

DT 22-MAY-2001 (first entry)

DE Human bcl-2alpha.

XX Human; Bax; cytostatic; immunosuppressive; immunostimulant; infection;

XX apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;

XX autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;

XX myocardial infarction; traumatic brain injury; ischaemia; bcl-2alpha;

XX neurodegenerative diseases; hepatitis; transplant rejection; toxemia;

XX lymphoproliferative disease; chromosome 18q21.3.

XX Homo sapiens.

XX US6184202-B1.

XX 06-FEB-2001.

XX 11-SEP-1997; 97US-00927326.

XX 26-AUG-1993; 93US-00112208.

XX 25-MAY-1994; 94US-00248819.

XX 10-NOV-1994; 94US-00337646.

XX (UNIW ) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 2001-256104/26.

XX Modulating apoptosis of a cell, useful in maintaining homeostasis in adult tissues, or treating proliferative or autoimmune diseases, comprises administering a bcl-2 polypeptide that interacts with a 21 kd bcl-2 associated X protein.

PS Disclosure; Col 29-30; 105pp; English.

XX The present invention relates to a method of modulating apoptosis of a cell. The method comprises administering to the cell an agent, comprising a Bcl-2 domain or Bcl-2 domain, capable of modulating formation of at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:Bax complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially useful in cancer therapy, and treating autoimmunity, immunodeficiency diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke, traumatic brain injury, neurodegenerative diseases, aging, ischaemia, toxemia, infection, hepatitis, transplant rejection, and lymphoproliferative diseases. The present sequence is human Bcl-2alpha, which was used in the method of the present invention. The human Bcl-2 gene is located on chromosome 18q21.3

SQ Sequence 239 AA;

Query Match 87.1%; Score 781.5; DB 4; Length 239;  
Best Local Similarity 73.4%; Pred. No. 4e-82;



CC regulatory proteins or for diagnostic assays. The present sequence is a  
 CC Bcl-2 antisense oligonucleotides associated protein sequence. Note: The  
 CC present sequence is included in the sequence listing but is not referred  
 CC to anywhere else in the specification

XX Sequence 239 AA;

Query Match 87.1%; Score 781.5; DB 5; Length 239;  
 Best Local Similarity 73.4%; Pred. No. 4e-82;  
 Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGVDNRRIIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
 |||||  
 DB 1 MAHAGRTGVDNRRIIVMKYIHYKLSQRYEWDAGDVGAAAPGAPAGCIFSOPGHTPHEA 60  
 |||||  
 QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
 |||||  
 DB 61 ASRDPVARTSPLOTAPAGAAAGPALSPPVPPVHLALROAGDDFSRRYRGDFAEMSSQLH 120  
 |||||  
 QY 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFFEFGVMCVESVNREMSPLVDNIALWMTEY 139  
 |||||  
 DB 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFFEFGVMCVESVNREMSPLVDNIALWMTEY 180  
 |||||  
 QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
 |||||  
 DB 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207  
 |||||

#### RESULT 12

ABG78477  
 ID ABG78477 standard; protein; 239 AA.

XX AC ABG78477;

DT 15-NOV-2002 (first entry)

DE Human Bcl2 mutant protein isoform 1 (Bcl2-iso1).

XX Human; Bcl2; BclX1; programmed cell death; apoptosis; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX WO200240530-A2.

XX 23-MAY-2002.

XX 15-NOV-2001; 2001WO-US045693.

XX 20-NOV-2000; 2000US-00716395.

XX (ABBO ) ABBOTT LAB.

XX Fesik SW, Petros AM, Yoon H, Nettesheim DG;

XX WPI; 2002-490141/52.

XX New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein,  
 PT useful in biological assays to identify substances that block the ability  
 PT of Bcl-2 to inhibit programmed cell death or apoptosis.

XX Claim 3; Fig 1; 36pp; English.

XX This invention relates to a novel mutant protein which is derived from a  
 CC wild type human Bcl-2 protein. The mutant is created by replacing a  
 CC sequence of amino acid residues comprising a flexible loop from the wild  
 CC type Bcl-2 protein with an amino acid sequence comprising at least two  
 CC acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue  
 CC shown in the specification. The invention also comprises an assay for  
 CC identifying substances that bind to the Bcl-2 protein. The protein  
 CC sequences of the invention are useful in biological assays to identify  
 CC substances that block the ability of Bcl-2 to inhibit programmed cell  
 CC death or apoptosis. The present sequence represents a human Bcl2 mutant

CC protein used in the invention

XX Sequence 239 AA;

Query Match 87.1%; Score 781.5; DB 5; Length 239;  
 Best Local Similarity 73.4%; Pred. No. 4e-82;  
 Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGVDNRRIIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
 |||||  
 DB 1 MAHAGRTGVDNRRIIVMKYIHYKLSQRYEWDAGDVGAAAPGAPAGCIFSOPGHTPHEA 60  
 |||||  
 QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
 |||||  
 DB 61 ASRDPVARTSPLOTAPAGAAAGPALSPPVPPVHLALROAGDDFSRRYRGDFAEMSSQLH 120  
 |||||  
 QY 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFFEFGVMCVESVNREMSPLVDNIALWMTEY 139  
 |||||  
 DB 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFFEFGVMCVESVNREMSPLVDNIALWMTEY 180  
 |||||  
 QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
 |||||  
 DB 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207  
 |||||

#### RESULT 13

ABB78197  
 ID ABB78197 standard; protein; 239 AA.

XX AC ABB78197;

XX 25-NOV-2002 (first entry)

XX Amino acid sequence of human bcl-2.

XX Antisense oligonucleotide; B cell lymphoma/leukemia-2 gene; bcl-2 gene;  
 KW cancer; lymphoma; leukemia; chemotherapeutic agent; bone marrow purging;  
 KW autoimmune disease.

XX Homo sapiens.

XX US6414134-B1.

XX 02-JUL-2002.

XX 28-NOV-2000; 2000US-00724426.

XX 22-DEC-1988; 88US-00288692.

XX 21-FEB-1992; 92US-00840716.

XX 20-SEP-1993; 93US-00124256.

XX 05-JUN-1995; 95US-00465485.

XX 18-MAY-1998; 98US-00080285.

XX 17-AUG-1999; 99US-00375514.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Reed JC;

XX WPI; 2002-641579/69.

XX Novel antisense oligonucleotide complementary to B cell lymphoma/leukemia  
 PT -2 mRNA, useful for inhibiting cancer cell growth, for treating  
 PT autoimmune disorders, and for ex vivo bone marrow purging.

XX Example 18; Col 39-42; 41pp; English.

XX The present sequence represents B cell lymphoma/leukemia-2 (bcl-2). The  
 CC specification describes antisense oligonucleotides complementary to B  
 CC cell lymphoma/leukemia-2 (bcl-2) mRNA. The antisense oligonucleotide is  
 CC useful for inhibiting cancer cell (lymphoma or leukemia cells) growth,  
 CC for increasing the sensitivity of cancer cells to cancer chemotherapeutic  
 CC agents, or for inducing cancer cell death alone or in combination with  
 CC any one or more cancer chemotherapeutic agents. It is also useful for

CC reducing the bcl-2 gene expression or impairing bcl-2 protein function,  
 CC for ex vivo bone marrow purging, for removing residual malignant cells  
 CC from the bone marrow, for inhibiting cancer of neoplastic cell growth,  
 CC and for treating autoimmune disease  
 XX  
 SQ Sequence 239 AA;

Query Match 87.1%; Score 781.5; DB 5; Length 239;  
 Best Local Similarity 73.4%; Pred. No. 4e-82;  
 Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGD-----DVEENRTEAPE 45  
 Db 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGDVGAAAPGAAAPGIFSSQPGHTHPHA 60

Qy 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79  
 Db 61 ASRDPVARTSPLQTPAAPGAAAPGALSPPVPPVHLLALRQAGDDFSRRYRGDFAEMSSQLH 120

Qy 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVESVNRMSPLVDNIALWMTEY 139  
 Db 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVESVNRMSPLVDNIALWMTEY 180

Qy 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
 Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 14  
 ABB78196  
 ID ABB78196 standard; protein; 239 AA.  
 AC ABB78196;  
 XX  
 XX 25-NOV-2002 (first entry)  
 DT  
 DE Amino acid sequence of human bcl-2.  
 XX  
 XX Antisense oligonucleotide; B cell lymphoma/leukemia-2 gene; bcl-2 gene;  
 KW cancer; lymphoma; leukemia; chemotherapeutic agent; bone marrow purging;  
 KW autoimmune disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US6414134-B1.  
 PN  
 XX  
 XX 02-JUL-2002.  
 PD  
 XX  
 XX 28-NOV-2000; 2000US-00724426.  
 PF  
 XX  
 XX 22-DEC-1988; 88US-00288692.  
 PR  
 XX 21-FEB-1992; 92US-00840716.  
 PR  
 XX 20-SEP-1993; 93US-00124256.  
 PR  
 XX 05-JUN-1995; 95US-00455485.  
 PR  
 XX 18-MAY-1998; 98US-00080285.  
 PR  
 XX 17-AUG-1999; 99US-00375514.  
 XX  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 PA  
 XX  
 XX Reed JC;  
 PI  
 XX  
 XX WPI; 2002-641579/69.  
 DR  
 XX N-PSDB; ABQ78196.  
 XX  
 XX Novel antisense oligonucleotide complementary to B cell lymphoma/leukemia  
 PT -2 mRNA, useful for inhibiting cancer cell growth, for treating  
 PT autoimmune disorders, and for ex vivo bone marrow purging.  
 XX  
 XX Example 18; Col 37-40; 41pp; English.  
 PS  
 XX The present sequence represents B cell lymphoma/leukemia-2 (bcl-2). The  
 CC specification describes antisense oligonucleotides complementary to B  
 CC cell lymphoma/leukemia-2 (bcl-2) mRNA. The antisense oligonucleotide is

CC useful for inhibiting cancer cell (lymphoma or leukemia cells) growth,  
 CC for increasing the sensitivity of cancer cells to cancer chemotherapeutic  
 CC agents, or for inducing cancer cell death alone or in combination with  
 CC any one or more cancer chemotherapeutic agents. It is also useful for  
 CC reducing the bcl-2 gene expression or impairing bcl-2 protein function,  
 CC for ex vivo bone marrow purging, for removing residual malignant cells  
 CC from the bone marrow, for inhibiting cancer of neoplastic cell growth,  
 CC and for treating autoimmune disease  
 XX  
 SQ Sequence 239 AA;

Query Match 87.1%; Score 781.5; DB 5; Length 239;  
 Best Local Similarity 73.4%; Pred. No. 4e-82;  
 Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGD-----DVEENRTEAPE 45  
 Db 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGDVGAAAPGAAAPGIFSSQPGHTHPHA 60

Qy 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79  
 Db 61 ASRDPVARTSPLQTPAAPGAAAPGALSPPVPPVHLLALRQAGDDFSRRYRGDFAEMSSQLH 120

Qy 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVESVNRMSPLVDNIALWMTEY 139  
 Db 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVESVNRMSPLVDNIALWMTEY 180

Qy 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
 Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 15  
 ABB75986  
 ID ABB75986 standard; protein; 239 AA.  
 AC ABB75986;  
 XX  
 XX 12-JUL-2002 (first entry)  
 DT  
 DE Protein sequence.  
 XX  
 KW B cell lymphoma/leukemia-2; bcl-2; oncogene; antisense; lymphoma;  
 KW leukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;  
 KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;  
 KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;  
 KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;  
 KW head and neck cancer; brain cancer; cytostatic; human; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200217852-A2.  
 PN  
 XX  
 XX 07-MAR-2002.  
 PD  
 XX  
 XX 23-AUG-2001; 2001WO-US026414.  
 PF  
 XX  
 XX 25-AUG-2000; 2000US-0227970P.  
 PR  
 XX 29-SEP-2000; 2000US-0237009P.  
 PR  
 XX 10-NOV-2000; 2000US-00709170.  
 XX  
 XX (GENT-) GENTA INC.  
 PA  
 XX  
 XX Warrel RP, Klem RE, Fingert H;  
 PI  
 XX  
 XX WPI; 2002-371796/40.  
 DR  
 XX N-PSDB; ABL54167.  
 XX  
 XX Treating or preventing cancer, tumors and carcinomas, comprises  
 PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at  
 PT high doses for short period for time with one or more cancer  
 PT therapeutics.  
 XX

PS Disclosure; Page 61; 64pp; English.

XX The present invention is related to the use of a B cell  
CC lymphoma/leukaemia-2 (bcl-2) antisense oligonucleotide, particularly  
CC G3139 (see ABL54148), to treat and prevent bcl-2 related disorders.  
CC Administration at high doses results in significant therapeutic  
CC responses, including low toxicity, high tolerance and prolonged survival.  
CC Administration at high doses for short periods of time (less than 14  
CC days) also provides significant therapeutic responses in the treatment of  
CC cancer. The bcl-2 antisense oligomer may also be used to increase the  
CC sensitivity of a subject to cancer therapeutics, and in combination with  
CC hormone treatment or gene therapy. Conditions that may be treated or  
CC prevented include cancer of the haematopoietic system, skin, bone and  
CC soft tissue, reproductive system, genitourinary system, breast, endocrine  
CC system, brain, central nervous system, peripheral nervous system, kidney,  
CC lung, respiratory system, thorax, gastrointestinal and alimentary canal,  
CC lymph nodes, pancreas, hepatobiliary system, or cancer of unknown primary  
CC site, non-Hodgkin's lymphoma, Hodgkin's lymphoma, leukaemia, colon  
CC carcinoma, rectal carcinoma, pancreatic, breast, ovarian, prostate,  
CC cervical, testicular, head and neck or brain cancer, renal cell  
CC carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, lung  
CC carcinoma, bladder carcinoma and melanoma (all claimed). Note: The  
CC present sequence is given in the Sequence Listing from the present  
CC invention but the Seq ID No. is not referred to within the specification  
XX

SQ Sequence 239 AA;

Query Match 87.1%; Score 781.5; DB 5; Length 239;  
Best Local Similarity 73.4%; Pred. No. 4e-82;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;  
  
QY 1 MAHAGTGYDNREIVMKYIHYKLSQGYEWDAGD-----DVEENRTEAPE 45  
Db |||||||||||||||||||||||||||||||||||||||||||||||||  
1 MAHAGTGYDNREIVMKYIHYKLSQGYEWDAGDVGAAAPGAAPAGPISFSGPCHTPHPA 60  
  
QY 46 GTES-----EVVHLALRQAGDDFRRYRGDFAEMSSQLH 79  
Db |||||||||||||||||||||||||||||||||||||||||||||||||  
61 ASRDPVARTSPLQTPAAPGAAGPALSPPVPVHVHLALRQAGDDFRRYRGDFAEMSSQLH 120  
  
QY 80 LTPFTARGFATVVEELFRDGVNMGRIVAFFEGGYMCVSVNREMSPLVDNIALWMTEY 139  
Db |||||||||||||||||||||||||||||||||||||||||||||||||  
121 LTPFTARGFATVVEELFRDGVNMGRIVAFFEGGYMCVSVNREMSPLVDNIALWMTEY 180  
  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
Db |||||||||||||||||||||||||||||||||||||||||||||||||  
181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

Search completed: December 30, 2006, 12:07:32  
Job time : 202 secs

This Page Blank (uspto)